

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 29, 2005, 16:53:09 ; Search time 29 Seconds
(without alignments)
1341.109 Million cell updates/sec

Title: US-09-857-581b-66

Perfect score: 2389

Sequence: 1 MLELALGLXVIALFXHLR.....AHSLVVCPLRIGVASKLLS 521

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2250	94.2	521	3	US-08-948-564-14
2	944.5	39.5	512	4	US-09-672-785-4
3	940.5	39.4	506	4	US-09-672-785-2
4	921.5	38.6	506	4	US-09-672-785-8
5	651	27.2	513	3	US-09-351-229-4
6	637.5	26.7	508	4	US-09-142-108C-17
7	629	26.3	495	4	US-09-689-783A-2
8	626	26.2	512	4	US-09-142-108C-6
9	623	26.1	513	4	US-09-142-108C-15
10	618.5	25.9	496	3	US-09-292-768-2
11	618.5	25.9	496	3	US-09-292-768-66
12	616.5	25.8	496	3	US-08-881-784-1
13	616.5	25.8	500	3	US-09-292-768-4
14	616.5	25.8	500	3	US-09-292-768-68
15	616.5	25.8	512	4	US-09-142-108C-2
16	615.5	25.8	500	3	US-09-292-768-70
17	613.5	25.7	496	3	US-09-292-768-64
18	613.5	25.7	500	3	US-08-881-784-9
19	608	25.4	502	3	US-09-499-302A-2
20	605.5	25.4	496	3	US-09-172-339-6
21	602.5	25.2	471	3	US-09-126-420A-20
22	599.5	25.1	498	5	US-09-292-768-6
23	592	24.8	508	4	US-09-142-108C-19
24	590.5	24.7	500	4	US-09-142-108C-4
25	590	24.7	517	4	US-09-142-108C-21
26	583	24.4	516	3	US-08-948-564-12
27	574	24.0	496	1	US-08-313-075A-50

28	574	24.0	496	4	US-09-142-108C-41
29	572	23.9	502	3	US-09-499-302A-4
30	570.5	23.9	510	3	US-08-606-505B-66
31	570.5	23.9	510	3	US-09-616-990-66
32	567	23.7	476	4	US-09-142-108C-23
33	566.5	23.7	476	1	US-08-313-075A-30
34	564	23.6	523	3	US-08-606-505B-67
35	564	23.6	523	3	US-09-616-990-67
36	563.5	23.6	506	1	US-08-313-075A-38
37	563.5	23.6	506	3	US-08-606-505B-65
38	563.5	23.6	506	3	US-09-616-990-65
39	562.5	23.5	513	4	US-09-142-108C-42
40	559.5	23.4	529	4	US-08-615-192A-405
41	556.5	23.3	490	2	US-09-126-420A-16
42	556.5	23.3	520	2	US-09-091-432-2
43	556.5	23.3	520	4	US-09-387-663-2
44	556.5	23.3	520	4	US-09-214-139B-4
45	555.5	23.3	510	3	US-08-948-564-4

ALIGNMENTS

RESULT 1

US-08-948-564-14
; Sequence 14, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminsky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/948,564
; APPLICATION NUMBER: 800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-564-14

Query Match 94.2%; Score 2250; DB 3; Length 521;

Best Local Similarity 86.6%; Pred. No. 3.1e-273;

Matches 451; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1 MLELALGLXVIALFXHLRPTTAXSALRHLNPPSPXPRLPFTIGHXHLKDLLHYAX 60

Db 1 MLELALGLVIALFLHLRPTTAKSALRHLNPPSPKPRLPFTIGHHLKDLLHYAL 60

Qy 61 IDLSKKGHPFLPSXXFGSMPTVWASTPELFLKXQXATSFXTFQTSAXRXLTYDXXVA 120
Db 61 IDLSKKGHPFLPSXXFGSMPTVWASTPELFLKXQXATSFXTFQTSAXRXLTYDSSVA 120
Qy 121 XXPGPYWKFVRKLIIMNDLXNATTNNKRLPLRTQQTFRXLRXMAQXAEAKPLDXTBELL 180
Db 121 MVPGPYWKFVRKLIIMNDLXNATTNNKRLPLRTQQTFRXLRXMAQXAEAKPLDXTBELL 180
Qy 181 KWNSTYSMMXKLGBAEIRDIARVILKXGEYSLTDFIXPLKXKLVGKYKRRIDDIILNKF 240
Db 181 KWNSTYSMMXKLGBAEIRDIARVILKXGEYSLTDFIXPLKXKLVGKYKRRIDDIILNKF 240
Qy 241 DPVVERVVKRRXIVRRRNXGEXXGKSGVXLDTLLEFAEDTETXIKTKXXIXGLVVD 300
Db 241 DPVVERVVKRRXIVRRRNXGEXXGKSGVXLDTLLEFAEDTETXIKTKXXIXGLVVD 300
Qy 301 XFSAGDSTAXXTWALAEILNPNKVLXAREEYXSVVGDVDTQNLPIYRAIVK 360
Db 301 XFSAGDSTAXXTWALAEILNPNKVLXAREEYXSVVGDVDTQNLPIYRAIVK 360
Qy 361 ETRFMHPPLPVKXKXEBCKXGKXVXPGALXXFNWQVXKXKXWDRPSEKXRPFL 420
Db 361 ETRFMHPPLPVKXKXEBCKXGKXVXPGALXXFNWQVXKXKXWDRPSEKXRPFL 420
Qy 421 TXABGEAXXLDLRCXHFQLLPFGSGRXCPCVXLATSGXATLLASLIQCFDQVLGPOGO 480
Db 421 TXABGEAXXLDLRCXHFQLLPFGSGRXCPCVXLATSGXATLLASLIQCFDQVLGPOGO 480
Qy 481 ILKXGDAKXWEEERAGLTVPRHSLVCVPLARIGVASKLLS 521
Db 481 ILKXGDAKXWEEERAGLTVPRHSLVCVPLARIGVASKLLS 521

RESULT 2

US-09-672-785-4
; Sequence 4, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Torenia hybrida
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-09-672-785-4

Query Match 39.5%; Score 944.5; DB 4; Length 512;
Best Local Similarity 38.9%; Pred. No. 2.3e-109;
Matches 193; Conservative 94; Mismatches 182; Indels 27; Gaps 8;

Qy 33 PNPPSPXPRLPFTGHXHLKDKLLHYAXIDLKXHGFLFSXXFGSMPTVWASTPELFLK 92
Db 29 PSPPGPL-SLPIITGHLLGLPR-LHHTFHFSLKYGFLQLKLSIPCVVASTPELAREF 86

Qy 93 LOXKEATSPXTRFQTSAXRXLTYDXXVAXXPGPYWKFVRKLIIMNDLXNATTNNKRLPLR 152
Db 87 LKTYNE-LAFSSRRKHSTAIIDIVTYDSSFAFSPYGPYKYLKKUCTYELLGARNLGHFQPIR 145
Qy 153 TOIRKXLRMAQXAEAKPLDXTTELLKWNXNSTXSMXL-----GEAEETIRDIARE 204
Db 146 NLEVRSPQLLMMHKSFKGESVNVTDVLRVLTNSVISHMMLISRCSEDEGDAEAARTVIRE 205
Qy 205 VLKIXGEYSLTDFIXPLKXKLVGKYKRRIDDIILNKFDPVVERVVKRRXIVRRRNXGEXX 264
Db 206 VTQIFGEFVDVTDIIFWCKKFDLQGIKKRSEDIORRYDALLEKTIISDRER--SRQNRDKH 263
Qy 265 EG--EYSGVXKLTLEFAEDTETXIKTKXXIXGLVVDXFSAGDSTAXXTWALAEIL 321
Db 264 GGGNNEAKDFLMDLQVMESEGTVEKFTREHLKALILDFDTAGTDTTATATWALAEIL 323
Qy 322 NPNKVLXAREEYXSVVGDVDTQNLPIYRAIVKTRFMHPPLPVVKKXCKBECK 381
Db 324 NPNVLKKAQEEISRIGTKRIVQESDAPDPLVQLAIKETFRLHPPLPMLSRKSTSDCT 383
Qy 382 INKXVPEGALXXFNWQVXKXKXWDRPSEKXRPFLFTYABGEAXXLDLRCXHFQLLP 441
Db 384 VNGYKIQAKSLLEFVNISIGRNPYWESEPMERPERFLEKGRE----SIDVKGQHFELLP 439
Qy 442 FSGSRXCPCVXLATSGXATLLASLIQCFDQVLGPOGOILKXGDAKXWEEERAGLTVPR 501
Db 440 FGTRRGCPGMLAIEVSVIIGTMVQCDF-----WKLADSGNNVDMTERSGLTAPR 492
Qy 502 AHSVLVCVPLARIGVAS 517
Db 493 AFDVLCRLYPRVDPAT 508

RESULT 3
US-09-672-785-2
; Sequence 2, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-09-672-785-2

Query Match 39.4%; Score 940.5; DB 4; Length 506;
Best Local Similarity 39.8%; Pred. No. 7.1e-109;
Matches 196; Conservative 86; Mismatches 185; Indels 25; Gaps 9;

Qy 30 RHLNPPSPXPRLPFTGHXHLKDKLLHYAXIDLKXHGFLFSXXFGSMPTVWASTPELFL 89
Db 24 RRKTRPPGPL-ALPLIGHLLGLPK-LHHTFHQFSQRYGLIQLGLSGVPCVVASTPELA 81

Qy 90 KLFQXKXEAFTXTRFQTSAXRXLTYDXXVAXXPGPYWVFRKLIIMNDLXNATTVXNLR 149
Db 82 REFLKTHE-LDFSRKHSTAIIDIVYDSSFAFAPYGPYKFIKKLCTYELLGARNLGHFQ 140
Qy 150 PLRTQOIRKXLRXMAQXAEAKPLDXTEELLKXNXTXSMXKL-----GEAEERDI 201
Db 141 PIRALEVNSFURILYEKTEQKQSVNTEELVKLTNSVISHMMLSGIRCSGTEGEAEVARTV 200
Qy 202 AREVLKIXGEYSLTDFIXPLKXKLVGKYEKRIDDILNKFDPVVERVIKRRXIVRRRXNG 261
Db 201 IREVTQIFGEFVSDIWLCKNFDFQIGIRKSEDIQRRYDALLEKIITDREK--QRRTHGGG 259
Qy 262 EXXGEGXGVKLDYLLFAEDETXEIKITKXIXGLVVDXPSAGXDSTAXXTWALAEILI 321
Db 260 GGGGGEVKD-FDMLLDVMESEKSEVEFTRHLKALILDFFTAGTDTTATTEWAI AEILI 318
Qy 322 NNPLVXXABEEXYSVVGKDXLVDVDTQNLPIYRAIVKETFRRMHPDLPVVKRCKXEECX 381
Db 319 SNPNVLKKAQEEEMDKVIGSQRLQESDAPNLPYLNAIKETFRLLHPPIPLMTRKISIDVV 378
Qy 382 INGXXPEGALXXFNVMQVGDXXKXWDPRSEXPFRFLETXAEGEAXXLDLGRGXHFOLLP 441
Db 379 VNGVTIYAKTLFVNLMSGRNPNYMNPMFRPERFLEKX---TGSIDVKGQHFELLP 434
Qy 442 FGSGRXCPGVKXLTSGXATLLASLIQCFLQVLGPGQOILKGXDAKVSMEERAGLTVPR 501
Db 435 FGTRRGCPGMLLGMQBELSFIIGAMVQCFDWKL--PDGV-----KSVDMTERPGLTAPR 486
Qy 502 AHSLVCVPLARI 513
Db 487 ANDLVQQLVPR 498

RESULT 4

US-09-672-785-8

; Sequence 8, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Perilla frutescens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to directly convert flavanone to flavone

US-09-672-785-8

Query Match 38.6%; Score 921.5; DB 4; Length 506;
Best Local Similarity 38.9%; Pred. No. 1.7e-106;
Matches 190; Conservative 91; Mismatches 183; Indels 25; Gaps 8;

Qy 33 PNPPSPYRLPFPIGHXHLKXLLHYAXIDLKXKXGDLPSXXFGSMPTVASTPELFLP 92
Db 27 PYPGPPFP-LPIIHLHLGPR-LHQTFHDLISQRYGLMQLMQLRGLSIRCVIAASPELAKEC 84

Qy 93 LOXXEATSFYTRFQTSAXRXLTYDXXVAXXPGPYWVFRKLIIMNDLXNATTVXNLRPLR 152
Db 85 LKTHELV-FSSRKHSTAIIDIVYDSSFAFAPYGPYKFIKKLCTYELLGARNLAHFQIR 143
Qy 153 TQOIRKXLRXMAQXAEAKPLDXTEELLKXNXTXSMXKL-----GEAEERDIARE 204
Db 144 TLEVKSFLQILMRKSGESGFNVTEELVKLTNSVISHMMLSIRCSSETESEAEAAARTVIRE 203
Qy 205 VLKIXGEYSLTDFIXPLKXKLVGKYEKRIDDILNKFDPVVERVIKRRXIVRRRXNGEXX 264
Db 204 VTQIFGEFVSDIWLCKNFDFQIGIRKSEDIQRRYDALLEKIITDREK--QRRTHGGG 261
Qy 265 EGXSGVXKLDYLLFAEDETXEIKITKXIXGLVVDXPSAGXDSTAXXTWALAEILNPP 324
Db 262 GGGGGEVKD-FDMLLDVMESEKSEVEFTRHLKALILDFFTAGTDTTATTEWAI AEILNPP 321
Qy 325 XVLXXABEEXYSVVGKDXLVDVDTQNLPIYRAIVKETFRRMHPDLPVVKRCKXEECXING 384
Db 322 NVLKKAQEEIANIVGFRILQESDAPNLPYLQALIKETFRLLHPPIPLMARKSISDCVLDG 381
Qy 385 XVAPEGALXXFNVMQVGDXXKXWDPRSEXPFRFLETXAEGEAXXLDLGRGXHFOLLPFGS 444
Db 382 YNIPANTLLFVNLMSGRNPNKIWDYPTAFQPERFLEK-----EKAAIDVKGQHFELLPGT 437
Qy 445 GRXWCPGVKXLTSGXATLLASLIQCFLQVLGPGQOILKGXDAKVSMEERAGLTVPRAHS 504
Db 438 GRRGCPGMLLAIQEVVILIGTMIQCFOWL--PDG-----SGHVDMAERPGLTAPRETD 489
Qy 505 LVCVPLARI 513
Db 490 LFCRVVPRV 498

RESULT 5

US-09-351-229-4

; Sequence 4, Application US/09351229
; Patent No. 6380465
; GENERAL INFORMATION:
; APPLICANT: Barrett, Michael
; TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: P-1049
; CURRENT APPLICATION NUMBER: US/09/351,229
; CURRENT FILING DATE: 1999-07-11
; EARLIER APPLICATION NUMBER: 60/092,596
; EARLIER FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-351-229-4

Query Match 27.2%; Score 651; DB 3; Length 513;
Best Local Similarity 32.6%; Pred. No. 1.6e-72;
Matches 164; Conservative 89; Mismatches 200; Indels 50; Gaps 13;

Qy 35 PPSPYRLPFPIGHXHLKXLLHYAXIDLKXKXGDLPSXXFGSMPTVASTPELFLPLQ 94
Db 29 PPGPKP-WPTIIGNLNLNMGELPHRSMNELSKRYGLMQLMQLMFGSLPVVVGASAEAKFLK 86
Qy 95 XEATSPXTTQTSAXRXLTYD--XXVAXXPGPYWVFRKLIIMNDLXNATTVXNLRPLRT 153
Db 87 TNDAA-AFSDRPRFVAVGKYTAYDCSLWAPPEPVLROARRICATELFSATRLSEFHIRD 145
Qy 154 QOIRKXLRXMAQXAEAKPLDXTEELLKXNXTXSMXKLGE----- 194
Db 146 EEVVVMRLQLRQAAGRTVRLRDYLOML--ALGVISRLVGLKXKYMEEAADGEGSDAPAIT 203
Qy 195 ABEIRDIAEVLKIXGEYSLTDFIXPLKXKLVGKYEKRIDDILNKFDPVVERVI---KKR 251
Db 204 PASFRENVDEFFALHGAFFNIGDYIPWLDWLDLQGYVARMKMKARFGRFLERVLDVHNER 263


```

/ TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
/
/ TITLE OF INVENTION: LIMONENE HYDROXYLASES
/
/ FILE REFERENCE: wsur13463
/
/ CURRENT APPLICATION NUMBER: US/09/292,768
/
/ CURRENT FILING DATE: 1999-04-14
/
/ EARLIER APPLICATION NUMBER: 08/881,784
/
/ EARLIER FILING DATE: 1997-06-24
/
/ NUMBER OF SEQ ID NOS: 70
/
/ SOFTWARE: PatentIn Ver. 2.0
/

```


Patent No. 6194185
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Dupien, Shari L
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
FILE REFERENCE: weur13463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 68
LENGTH: 500
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-292-768-68

Query Match 25.8%; Score 616.5; DB 3; Length 500;
Best Local Similarity 25.6%; Pred. No. 3.36-68;
Matches 145; Conservative 91; Mismatches 207; Indels 47; Gaps 11;
Qy 35 PPSPKPLPFIHGHLLKDLKLLHYAXIDLKSKHGLPFSXXFGSMPTVVASTPELFLQ 94
Db 36 PPGP-PKPLIGHLLHLLWGLKQHALASVAKQGFVAHVQLGEVFSVLSREATKEAMK 94
Qy 95 XEATSFXTRPQTSAXXLTYD--XXVAXXPXGPVWVFXVKLIMDLNATVNXLRP 153
Db 95 LVD-PACADRPESTGTIMWYDNDIIIFSPYSVHWQRKICVSELLSARNVRSFGFIRQ 153
Qy 154 QOIRKXLRXMAQAEAKPLDXTTELLKWNSTXSMXKLG-----EAEIRDIAREVLKIX 209
Db 154 DEVSRLGLHRSAAAGEAVDLTRATLTCSIIICRAAFSGVIRDBEELVELVKDALSM 213
Qy 210 GEYSLTDFIXPLKXL-----KVGKYEKRIDDILNKFDPVVERVVKGRXIVRRXNG 261
Db 214 SGPELADMFSSKLLNLLCNWKSCLWRMRVRDAILAI--VEBHLKX----- 260
Qy 262 EXEAGESGV-XLDTLLEFADETXEIKITKXIXGLVVDXFSAGXOSTAXXTWALAE 320
Db 261 ---SGEFGGDIIDVLFPMQKDSQIKVPITTKAIFIDTFSAGTSTSTTTILWNAEL 317
Qy 321 INNPVLLXXAREEYSVVGVKDXLVDVDTQNLPIYIRAI VKETFRMHPPLPVKXCKXEC 380
Db 318 MRNPEVMAKQAEVRAALKGTDWDDVDELTKYKSVVRETMRMHPPIELIPRSCREC 377
Qy 381 XINGXVPEGALXXFNWQVGDXXKYWDPRSEKRPERFLETXAEGEAXXLDLGRXHPQL 440
Db 378 EVNGYTIIPNKARIMINWMSGRNPLYWEKPETPWPERF-----DQVSRDFMGNDPEFI 430
Qy 441 PFGSGRXCPCVXLATSGXATLLASLLOCFDVLGPGQQLKXGD-AKVSMEERAGLTV 499
Db 431 PFGAGRRICPGLNFGLANVEVPLAQLLYHFD-----WKLAEGMNPSMDMSEAEGLTG 483
Qy 500 PRAHSLVCVP 509
Db 484 IRKNLLVLP 493

RESULT 15
US-09-142-108C-2
Sequence 2, Application US/09142108C
Patent No. 6774285
GENERAL INFORMATION:
APPLICANT: Brugliera, Filippa
APPLICANT: Holton, Timothy A.
APPLICANT: Michael, Michael Z.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
FILE REFERENCE: 11658
CURRENT APPLICATION NUMBER: US/09/142,108C

CURRENT FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: P8386
PRIOR FILING DATE: 1996-03-01
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 512
TYPE: PRT
ORGANISM: Petunia x hybrida
US-09-142-108C-2
Query Match 25.8%; Score 616.5; DB 4; Length 512;
Best Local Similarity 30.7%; Pred. No. 3.4e-68;
Matches 153; Conservative 96; Mismatches 209; Indels 41; Gaps 13;
Qy 32 LPNPPSPXRLPFIHGHLLKDLKLLHYAXIDLKSKHGLPFSXXFGSMPTVVASTPELFLK 91
Db 31 LPLPPGPKP-WPIIGNLVHLGPK-PHQSTAAMAQTYGPLMYLKMGFVDVVVAASASVAAQ 88
Qy 92 FLQXXEATSFTRPQTSAXXLTYD--XXVAXXPXGPVWVFXVKLIMDLNATVNXLRP 150
Db 89 FLKTHDA-NFSSRPPNSGAEMAYNYQDUFVFPYGPWRMLRKICSVHLFSTKALDDFRH 147
Qy 151 LRTQOIRKXLRXMAQAEAKPLDXTTELLKWNSTXSMXKLG-----EAEIRDIAREVLKIX 197
Db 148 VRQDEVKTLTRALASAGQ--KPVKLGQLLVNCTTNALARVWLGKRVFADGSGDVPQAAE 205
Qy 198 IRDIAREVLKIXGEYSLTDFIXPLKXKVGKYEKRIDDILNKFDPVVERVVKGRXIVRR 257
Db 206 FKSMMVEMMVVAGVFNIGDFIPQLNMLDIOGVAAMKMLKHARFADFALTILEHKG--- 261
Qy 258 RXNGEXXEGEXSGVXLDTLLEFADETXEIKITKXIXGLVVDXFSAGXOSTAXXTW 315
Db 262 KIFGEMD-----LSTLISLKNDDADNDGKLTDEIKALLNLVFAVGTDTSSSTVEW 315
Qy 316 ALAELINNPVLLXXAREEYSVVGVKDXLVDVDTQNLPIYIRAI VKETFRMHPPLPV-VKR 374
Db 316 AIAELIRNPKILAAQAEIDKVVGRDLVGEGLDIAQLTYLEAIVKETFRMHPSTPLSLPR 375
Qy 375 KCXECXKXVPEGALXXFNWQVGDXXKYWDPRSEKRPERFLETXAEGEAXXLDLGR 434
Db 376 IASESCBINGYFTPKGSTLLNLYWAIARDPNAWADPLEFRPERFL---PGGEKPKVDVRG 432
Qy 435 XHFOLLPPFGSGRXCPCVXLATSGXATLLASLLOCFDVLGPGQQLKXGD-AKVSMEER 494
Db 433 NDFEVIFFGAGRRI CAGMNLGIRMVQLMIA TLHAFNWDLV--SGQL-----PEMLNNEEA 486
Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 487 YGLTLQRADEPLVVHPRRL 505

Search completed: April 29, 2005, 17:32:17
Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: April 29, 2005, 17:33:00 ; Search time 874 Seconds
(without alignments)
3628.930 Million cell updates/sec

Title: US-09-857-581B-66
Perfect score: 2389
Sequence: 1 MLELALGLXLVLFHXLRP.....AHSIVCVPLARIGVASKLLS 521

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO_pool/h/US9857581/runat_29042005_104824_21017/app_query.fasta_1.711
-DB=Published Applications NA -QFWT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blseqm2
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HRAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US9857581@cgn2_1.1.480 @runat_29042005_104824_21017
-NCPU=6 -ICPU=3 -NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOK=100
-LONG LOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	94.5	2258	1756	16	US-10-171-174A-9
2	94.5	2258	1756	16	US-10-104-706-1
3	2256	94.4	1709	17	US-10-310-154-367
4	2250	94.2	1824	18	US-10-659-755-1
5	2130	89.2	1974	18	US-10-739-930-3497
6	944.5	39.5	1730	17	US-10-411-115-3
7	944.5	39.5	1730	18	US-10-411-225-3
8	943.5	39.5	1724	17	US-10-411-115-1
9	943.5	39.5	1724	18	US-10-411-225-1
10	921.5	38.6	1770	17	US-10-411-115-7
11	921.5	38.6	1770	18	US-10-411-225-7
12	919.5	38.5	1841	17	US-10-424-599-6882
13	877.5	36.7	3328	17	US-10-424-599-78567
14	870	36.4	1842	17	US-10-424-599-120588
15	843	35.3	1906	17	US-10-424-599-101968
16	807.5	33.8	1740	18	US-10-437-963-48274
17	761.5	31.9	1650	18	US-10-437-963-21012
18	730.5	30.6	1893	18	US-10-437-963-67133
19	717	30.0	2278	17	US-10-424-599-100510
20	701.5	29.4	1719	17	US-10-424-599-115417
21	693	29.0	1308	17	US-10-260-238-1264
22	691.5	28.9	1825	17	US-10-425-114-24949
23	680.5	28.5	1915	18	US-10-425-115-89637
24	680.5	28.5	2233	18	US-10-739-930-2248
25	666.5	27.9	1930	18	US-10-425-115-94744
26	657	27.5	1633	18	US-10-437-963-38374
27	651	27.2	1530	16	US-10-097-559-12
28	649.5	27.2	1922	17	US-10-425-114-27875
29	649.5	27.2	2008	18	US-10-425-115-94743
30	637.5	26.7	1660	19	US-10-669-962-16
31	637	26.7	5822	18	US-10-437-963-3724
32	634	26.5	1615	18	US-10-686-947-259
33	633.5	26.5	1610	18	US-10-686-947-197
34	633.5	26.5	1610	18	US-10-686-947-261
35	632.5	26.5	1657	18	US-10-686-947-195
36	631	26.4	1652	18	US-10-686-947-193
37	631	26.4	1862	18	US-10-437-963-46212
38	630.5	26.4	2081	17	US-10-424-599-2618
39	627	26.2	1617	18	US-10-686-947-267
40	626	26.2	1711	19	US-10-669-962-5
41	623	26.1	1576	18	US-10-686-947-149
42	623	26.1	1748	19	US-10-669-962-14
43	623	26.1	1988	17	US-10-424-599-2607
44	620.5	26.0	1647	18	US-10-437-963-10169
45	619	25.9	1566	18	US-10-686-947-191

ALIGNMENTS

RESULT 1

US-10-171-174A-9
; Sequence 9, Appli
; Publication No. US20030150012A1
; GENERAL INFORMATION:
; APPLICANT: Odell, Joan
; APPLICANT: Yu, Xiaodan
; TITLE OF INVENTION: OF AN ISOFLAVONOID-PRODUCING PLANT
; FILE REFERENCE: B1452 US NA
; CURRENT APPLICATION NUMBER: US/10/171.174A
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/297,981
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max

ALIGNMENTS

Alignment Scores: 1756

Alignment Scores: 1756

Score: 2258.00 Matches: 452
Percent Similarity: 86.76% Conservativity: 0
Best Local Similarity: 86.76% Mismatches: 69
Query Match: 94.52% Indels: 0
DB: 16 Gaps: 0

US-09-857-581B-66 (1-521) x US-10-104-706-1 (1-1756)

Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
Db 67 ATGTTGCTGGAACCTGCACCTGGTTGTTGTTGTTAGCTTTGTTCTGCACCTTGGCTCC 126
Qy 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
Db 127 ACACCAAGTGCAAAATCAAAAGCACTTCGCCACCTCCCAAAACCTCCCAAGGCCCAAGCCT 186
Qy 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla 60
Db 187 CGTCTTCCCTTCATTTGGCCACCTTCACCTCTTAAAGATAAACTTCTCCACTATGCACTC 246
Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
Db 247 ATCGATCTCTCAAAAGCATGGCCCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 306
Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
Db 307 GTCGTTGCTCCACCCCTGAGTTGTTCAAGCTCTTCTCTCAAAACCCACGAGGCCAATTC 366
Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
Db 367 TTCAACCAAGAGTTTCCAAACCTCTGCCATAAGACGCCCTCACTTACGACCACTCTGTGCC 426
Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu*** 140
Db 427 ATGTTTCCATTCGACACCTTACTGGAAGTTCGTGAGGAGCTCATCATGACGACCTTCTC 486
Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
Db 487 AACGCCACCCGCTCAACAGCTCAGGCTTGGAGGCTTGGAGGCCCAACAGATCCGCAAGTCT 546
Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
Db 547 AGGTTTATGGCCCAAGCGCAGAGGCCCGCAGAGGCCCTTGACGTCACCGAGGAGCTTCTC 606
Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
Db 607 AAATGGACCAACACACACCATCTCCATGATGATGTCGCGGAGGCTGAGGAGATCAGAGAC 666
Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
Db 667 ATCGCTCGCAGGTTCTTAAGATCTTCGGCGAATACAGACCTCACTGACTTTCATCTGGCCT 726
Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
Db 727 TTGAAGTATCTCAAGGTTGGAAGTATGAGAAGAGGATGTGATGATCATCTTTGAACAAGTTC 786
Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
Db 787 GACCTGTGTTGAAGGTCATCAAGAGCGCGCTGAGATCGTCAGAAGGAGGAAGAAC 846
Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
Db 847 GGAGAAGTTGTTGAGGCGAGGCCCGCGCTCTCTCTCGACACTTTGCTTGAATTCGCT 906
Qy 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
Db 907 GAGCAGCAGACCATGAGATCAAAATTAACCAAGGAGCAAAATCAAGGCGCTTGTGTGCGAC 966
Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTyrAlaLeuAlaGluLeu 320
Db 967 TTTTCTCTCGAGGAGCAGATTCACAGCGGTGCCAACAGAGTGGGCTATGGCAGAGCTC 1026
Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340

Db 1027 ATCAACAAATCCAGGGTGTTCACAAAGGCTCGTGAGGAGGTCTACAGTGTGTGGGCAAA 1086
Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleAtqAlaIleValLys 360
Db 1087 GATAGACTCGTTGACGAAGTTGACACTCAAAACCTTCTTACATTTAGGGCCATTTGTGAAG 1146
Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
Db 1147 GAGACATTCGAATGCACCCACCACTCCCACTGGTGTCAAAAGAAAGTGCACAGAAGAGTGT 1206
Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1207 GAGATTAAATGGGTATGTGATCCCAAGAGGAGCATTTGGTTCTTTTCAATGTTTGGCAAGTA 1266
Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1267 GGAAGGACCCCAATACTGGGACAGACCATCAGAAATTCGTCGCCGAGAGTTCTTAGNA 1326
Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db 1327 ACTGGTCTGAAGGGGAGCAGGGCCCTCTTGATCTTAGGGGCCAGCATTTCCAACTCCTC 1386
Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1387 CCATTTGGTCTGGGAGGAGAAATGTGCCCTGTCTCAATTTGGCTACTTTCAGGAATGGCA 1446
Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
Db 1447 ACATCTTGTGATCTCTTATCCAAATGCTTTGACCTGCAAGTGTGGGGCCCTCAAGGACAA 1506
Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
Db 1507 ATATTGAAGGTGATGATGCCAAGTTAGCATGGAAGAGAGAGCTGGCTCAGAGTTCCA 1566
Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaLysLysLeuLeu 520
Db 1567 AGGCACATAGTCTGTTGTTGTTGCCACTTGCAGGATCGCGTGTGCATCTTAAACTCCTT 1626
Qy 521 Ser 521
Db 1627 TCT 1629

RESULT 3
US-10-310-154-367
; Sequence 367, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong


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QY      521 Ser 521      |||
Db      1614 TCT 1616

RESULT 5
US-10-739-930-3497
; Sequence 3497, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 39-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 3497
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER3333_17
US-10-739-930-3497

Alignment Scores:
Pred. No.: 1.17e-299      Length: 1974
Score: 2130.00           Matches: 430
Percent Similarity: 83.11%      Conservative: 3
Best Local Similarity: 82.53%    Mismatches: 78
Query Match: 89.16%             Indels: 10
DB: 18                      Gaps: 1

US-09-857-581B-66 (1-521) x US-10-739-930-3497 (1-1974)

QY      1 MetLeuLeuGluValLeuAlaLeuGlyLeu**ValLeuAlaLeuPhe***HisLeuArgPro 20
Db      259 ATGTTGCTGGAACCTTGACCTTGGTTGTTGTTAGTCTGGTTCTGCACTTGGCTGCC 318

QY      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
Db      319 ACACCAAGTGCACAAATCAAAAGCACCTTGCACCTCCCAACCCCTCCAAAGCCCT 378

QY      41 ArgLeuProPheLeuGlyHis***HisLeuLysAspLysLeuLeuHisTyrAla*** 60
Db      379 CGTCCTCCCTTCATTGGGCACTTCACTCTTAAAGATTAACCTTCCACTATGCACTC 438

QY      61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
Db      439 ATCGATCTCTCCAAAAGCATGGCCCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 498

QY      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
Db      499 GTCCGGGGCTCCACCCCTGAGTTGTTCAAGCTCTTCTCCAAACCCACAGAGGAACCTTC 558

QY      101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
Db      559 TTCACACAGAGTTTCCAAACCTCTGCCATAGAGCCCTCACTTACGACAACTCTGTGGCC 618

QY      121 *****Pro***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu** 140
Db      619 ATGGTTCCATTGGACCTTACTGGAAGTTCTGAGGAAGCTCATCATGAACGACCTTCTC 678

QY      141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnLeuArgLys***Leu 160
Db      679 AACGCCACCAACCGCAACAGCTCAGGCCCTTGGAGGACCCCAACAGATCCCGAAGTTCCCT 738

QY      161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
Db      739 AGGGTTATGGCCCAAGCGCAGAGGCCCTTTCAGCTCACCGAGGAGCTTCTC 798

QY      181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluLeuArgAsp 200
Db      799 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGCGAGGCTGAGATGATCAGAGAC 858

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RESULT 6

US-10-411-115-3
; Sequence 3, Application US/10411115
; Publication No. US20040003431A1

521 Ser 521
|||
1789 TCT 1791

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QY      201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
Db      859 ATCGCTCGCGAGGTTCTTAAGATCTTCGGCGAATACAGCCTCACTGACTTCATCTCGGCT 918

QY      221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
Db      919 TTGAAGTATCTCAAGGTTGGAAGATGATGAGAGAGGATGATGACATCTTGAACAGTTC 978

QY      241 AspProValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
Db      979 GACCCCTGTCTCAAGGTCATCAAGAGCCGCTGAGATCTGCAGAGGAGAGAAAC 1038

QY      261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
Db      1039 GGAGAAAGTTGTTGAGGGCGAGGCGGCTCTCTCCGACACATTTGTTGAATTCGCT 1098

QY      281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
Db      1099 GAGGACGACCATCGAGATCAAAATTCACCAAGGAGCAAAATCAAGGGCTTGTGTGCGAC 1158

QY      301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
Db      1159 TTTTCTCTGCGAGGACAGATTCACAGCGGTGGCAACAGAGTGGGCATTTGCAGAGCTC 1218

QY      321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
Db      1219 GTGAGGAGCTTACA-----GCTGTTGTGGCAAA 1248

QY      341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db      1249 GATAGACTCGTTGACGAAGTTGACACTCAAAACCTTCTTACATTAGGGCCATTGTGAAG 1308

QY      361 GluThrPheArgMethHisProProLeuProValValLysArgLysCys***GluGluCys 380
Db      1309 GAGACATTCGAATGCACCCACCTCCACAGTGGTCCAAAGAAAGTGCACAGAAAGTGT 1368

QY      381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db      1369 GAGATTAAATGGGTATGTGATCCAGAGGGAGCATTTGTTCTTTCAATGTTTGGCAAGTA 1428

QY      401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db      1429 GGAAGGGACCCCAAAATACTGGGACAGACCATCAGAAATTCCTCCCGAGAGGTTCTTAGAA 1488

QY      421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db      1489 ACTGGTGTCTGAAGGGAAGCAGGGCCCTCTTGATCTTAGGGGGCCAGCATTTCCAACCTCC 1548

QY      441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db      1549 CCATTTGGGTCTGGGAGGAGAAATGTCCCTGGGCTCAATTTGGTACTTTCAGGAATGGCA 1608

QY      461 ThrLeuLeuAlaSerLeuLeuGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
Db      1609 ACATCTTGTGCATCTCTTATCCAAATGCTTTGACCTGCAAGTGTCTGGGGCCCTCAAGGACAA 1668

QY      481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
Db      1669 ATATTCAAGGAGGATGATCCCAAGTTAGCATGGAAGAGAGAGCTGGCTTCACAGTTCCA 1728

QY      501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
Db      1729 AGGGCACATAGTCTCGTTTGTGTCTCCACTTGCAGAGGATCGGCGTTGCATCTAAACTCCTT 1788

QY      521 Ser 521  
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1789 TCT 1791

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RESULT 8

US-10-411-115-1
 ; Sequence 1, Application US/10411115
 ; Publication No. US20040003431A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mizutani, Masako
 ; APPLICANT: Kasumi, Takaaki
 ; APPLICANT: Ayabe, Shin-ichi
 ; APPLICANT: Akashi, Tomoyoshi
 ; TITLE OF INVENTION: Genes Coding for Flavone Synthases
 ; FILE REFERENCE: 001560-383
 ; CURRENT APPLICATION NUMBER: US/10/411.115
 ; CURRENT FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: US/09/672,785
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/04379
 ; PRIOR FILING DATE: 2000-01-30
 ; PRIOR APPLICATION NUMBER: PCT/JP00/00490
 ; PRIOR FILING DATE: 1999-01-28
 ; PRIOR APPLICATION NUMBER: JP 11-205229
 ; PRIOR FILING DATE: 1999-01-19
 ; PRIOR APPLICATION NUMBER: JP 11-22427
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1724
 ; TYPE: DNA
 ; ORGANISM: Antirrhinum majus
 ; FEATURE:
 ; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
 ; OTHER INFORMATION: activity to directly convert flavanone to flavone
 US-10-411-115-1

Alignment Scores:

Pred. No.: 1.84e-126 Length: 1724
 Score: 943.50 Matches: 198
 Percent Similarity: 57.31% Conservative: 88
 Best Local Similarity: 39.68% Mismatches: 179
 Query Match: 39.49% Indels: 34
 DB: 17 Gaps: 9

US-09-857-581B-66 (1-521) x US-10-411-115-1 (1-1724)

Qy 33 ProAsnProSerPro***Pro-Arg-----LeuPr 43
 Db 87 CTTCAACCTCTTAACCGCCACCGCCGCAAGACCGCCGCCCATTTAGCCCTCCC 146
 Qy 43 oPheileGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLe 63
 Db 147 CTTAATAGGCACATTACACCTCTCTGGGCCAAG---CTCCACACACCTTCCACCAATT 203
 Qy 63 uSerLysHisGlyProLeuPheSer*****PheGlySerMetProThrValVal 83
 Db 204 CTCCCAACCGCTACGGCCGCTCATCCAGCTCTACCTCGGCTCCGTCGCTCGC 263
 Qy 83 aSerThrProLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***Th 103
 Db 264 TTCCACGCCCGCAATTCCTCAAGACGCAAG---CTCGACTTCTCGTC 320
 Qy 103 rArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla***Pr 123
 Db 321 CCGCAAGCACTCCACCGCCATCGACATCGTCAGTACGACTCTCTCGTTCGCTTCGCGCC 380
 Qy 123 o***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu***AsnAlaTh 143
 Db 381 GTACGGCGCTACTCGAAATTCATCAAGAAATTTATGACTTACGAGCTACTCGGTGCGC 440
 Qy 143 rThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***Me 163
 Db 441 GAACCTTGAGCCATTTCCAGCCCATTTAGAGCTTTGAGGTCAACAGTTTCTTTGAGAATTT 500
 Qy 163 tAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp** 183

Db 501 GTACGAGAAACACAGACAGAAACACAGAGTGTAAATGTGACTGAGGAGCTTGTGAAGCTGAC 560
 Qy 183 *AsnSerThr***SerMetMet***Leu-----GlyGluAl 195
 Db 561 GAGTAATGTGATCAGTAACATGATGTTGGGATCAGGTGTCGGGGACGGAAGGGAGGC 620
 Qy 195 aGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuTh 215
 Db 621 GGAGTGGCGGAGCGGTGATAGGGAGGTGACCCAGATATTTGGGAGTTGATGTGTC 680
 Qy 215 rAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAs 235
 Db 681 GGAGATTGTTGTTGTAAGAAATTTGGATCTCGAGGGATTTAGGAAGAGTCCGAGGA 740
 Qy 235 pIleLeuAsnLysPheAspProValValGluArgValIleLysLysArg***IleVa 255
 Db 741 TATTAGGAGGATGATGCTTTGTTGGAGAAATTTATTAGTATAGGGAGAGGTTG-- 798
 Qy 255 lAtgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspTh 275
 Db 799 -AGTTGAGGGGGGTGTTGGTGGAGGGGTGGAGAGTGAAGAT---TTTTTGGATAT 854
 Qy 275 rLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile** 295
 Db 855 GTTGTGGATGTCATCGAGAGTGAAGAAATCGAGGTGGAGTTTACGAGGAGCATCTCAA 914
 Qy 295 *GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTr 315
 Db 915 AGCTTTGATTTGATTTCTTCACTGCGGTGACAGACACACACCAATTCACACAGAAATG 974
 Qy 315 pAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Ty 335
 Db 975 GGCATAGCAGAACTCATTTAGCAATCCAAATGTTACTCAAAAAGCTCAAGAGAGATGGA 1034
 Qy 335 rSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIl 355
 Db 1035 CAAAGTCATAGGATCAACAAAGTTGTTGCAAGATCCGACGCCCTAACTTGCCTTACCT 1094
 Qy 355 eArgAlaIleValLysGluThrPheArgMetHisProLeuProValValLysArgLys 375
 Db 1095 CAACGCGATCATAAAGAAACGTTCCGTCCTCCACCTCCCAATCCCATGCTCATAGAAA 1154
 Qy 375 sCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Ph 395
 Db 1155 ATCAATTTCTGACGTTGTTGTCACGGGTACACGATCCCTGCCAAAACGCTATTGTTGT 1214
 Qy 395 eAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPr 415
 Db 1215 CAACCTTTGGTCCATGGGAAGGAATCTTAACCTCTGGGAAATCCGATGGAGTTCCGACC 1274
 Qy 415 oGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly** 435
 Db 1275 CGAGAGGTTTCTCGAAGAAAGG-----ACCGGGTCGATAGACGTTAAAGGGCA 1322
 Qy 435 *HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAl 455
 Db 1323 GCATTTGAGTTGCTCGCTTTGGCAGGGCAGCGGGGCTCCCGGGGATGTTGTTAGG 1382
 Qy 455 aThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal 475
 Db 1383 CATCGAGGTTGTTTAGTATTATCGGGCTATGTCAGTGCAGTCTCGATTGGAAAATC- 1440
 Qy 475 uGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAl 495
 Db 1441 ----CCGATGGTGTG-----AAGTCGTCGATACGACCGAGCGGCC 1478
 Qy 495 aGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIle 513
 Db 1479 CGGTTGACGCTCCAGTGCCTCAATGATTTGGTGTGCAATTTGTTGCCACGAT 1533
 RESULT 9
 US-10-411-225-1

GENERAL INFORMATION:
 APPLICANT: Mizutani, Masako
 APPLICANT: Kasumi, Takaaki
 APPLICANT: Ayabe, Shin-ichi
 APPLICANT: Akashi, Tomoyoshi
 TITLE OF INVENTION: Genes Coding for Flavone Synthases
 FILE REFERENCE: 001560-383
 CURRENT APPLICATION NUMBER: US/10/411.115
 CURRENT FILING DATE: 2003-04-11
 PRIOR APPLICATION NUMBER: US/09/672,785
 PRIOR FILING DATE: 2000-09-29
 PRIOR APPLICATION NUMBER: PCT/JP00/04379
 PRIOR FILING DATE: 2000-01-30
 PRIOR APPLICATION NUMBER: PCT/JP00/00490
 PRIOR FILING DATE: 1999-01-28
 PRIOR APPLICATION NUMBER: JP 11-205229
 PRIOR FILING DATE: 1999-01-19
 PRIOR APPLICATION NUMBER: JP 11-22427
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 7

LENGTH: 1770
 TYPE: DNA
 ORGANISM: *Perilla frutescens*
 FEATURE:
 OTHER INFORMATION: Nucleotide sequence encoding a protein having an activity to directly convert flavanone to flavone
 US-10-411-115-7

Alignment Scores:
 Pred. No.: 3,13e-123 Length: 1770
 Score: 921.50 Matches: 190
 Percent Similarity: 57.46% Conservative: 91
 Best Local Similarity: 38.85% Mismatches: 183
 Query Match: 38.57% Gaps: 25
 DB: 17

US-09-857-581b-66 (1-521) x US-10-411-115-7 (1-1770)

Qy 33 ProAsnProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLys 52
 Db 99 CCTTACCTCCCGCGCGTTCCTCTCTCCCATCATCGGCCCATACACCTCTCTCGGG 155
 Qy 53 AspLysLeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer 72
 Db 156 CCGAGA---CTCCACCAAACTTCACAGATCTGCCAACGGTAGCGGCCCTTATGCAG 212
 Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe 92
 Db 213 CTCCGCTCGGGTTCATCCGCTGCTCATCTGCTCGCGGAGCTCGCCAAAGATGC 272
 Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
 Db 273 CTCAAGACACAGAGCTCGTC---TTCTCTCCCGCAAACTCCACCGCCCATTTGATATC 329
 Qy 113 LeuThrTyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheValArg 132
 Db 330 GTCCACCTACGATCATCTCTGCTCTCTCCCTACGGGCTTACTGGAATTCATCAAG 389
 Qy 133 LysLeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArg 152
 Db 390 AAATATGCACCTACGAGCTGCTCGGGCCCGGAATCTCGCCCACTTTTCAGCCCATCAGG 449
 Qy 153 ThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysPro 172
 Db 450 ACTCTCGAAGTCAAGTCTTCTCTCCAAATCTTATGCGCAAGGGTGAATCGGGGAGAGC 509
 Qy 173 LeuAsp***ThrGluGluLeuLysTrp***AenSerThr***SerMetMet***Leu 192
 Db 510 TTCAACGTGACTGAGGAGCTCGTGAAGCTGACGAGCAACGTCATATCATGATGCTG 569
 Qy 193 -----GlyGluAlaGluGluIleArgAspIleAlaArgGlu 204

Db 570 AGCATACGGTGTTCAGACGCGAGTTCGAGCGCGAGCGCGGAGCGTTCATTTCGGAG 629
 Qy 205 ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224
 Db 630 GTACGCGAGATATTTGGGAGTTCGAGCTCCGACATCATATGGCTTTGTAAAGACATTC 689
 Qy 225 LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProValVal 244
 Db 690 GATTTCCAAGGTATAAGGAAGCGTCCGAGATATCCAGAGAGATATGATGCTCTGCTG 749
 Qy 245 GluArgValIleLysLysArgArg***IleValArgArgArg***AenGlyGlu***** 264
 Db 750 GAGAAGATCATCCGACAGAGAGAAG-----CAGAGGCGGACCCAGCGCGCGGTGGC 803
 Qy 265 GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr 284
 Db 804 GCGCGCGGGAAGCCAGGATTTCTTGACATGTTCTCGACATAATCGAGAGCGGGA 863
 Qy 285 ***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAla 304
 Db 864 GCCAAGTTAAATTCAGAGGAGCATCTCAAAGCTTTGATTTCTGGATTTCTTCAACGCC 923
 Qy 305 Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro 324
 Db 924 GGCACCGACACGCGCGGATCGTGTGAATGGCGGATAGCAGAGTGTATCAACAATCCA 983
 Qy 325 ***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuVal 344
 Db 984 AATGTGTGAAGAAAGCTCAAGAGATGTCGAACATCTCGATTCGATTCGACAGATTCG 1043
 Qy 345 AspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArg 364
 Db 1044 CAAGAATCCGAGCGCCCAATCTGCTTCAAGCCCTCATCAAGAAACATTTCCGG 1103
 Qy 365 MethHisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly 384
 Db 1104 CTCACCCCTCCAATCCCAATGCTCGCGAGGAATTCGATCTCGGACTGCTCATCGACGC 1163
 Qy 385 ***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp*** 404
 Db 1164 TACATGATTCGCGCAACACGCTGCTCTTCTGTCACCTCTGCTCCATGGGCGGACCT 1223
 Qy 405 LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGlu 424
 Db 1224 AAATCTGGGACTACCCGACGCGCTTCAGCGGAGAGGTTTCTGGAGAAG----- 1274
 Qy 425 GlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySer 444
 Db 1275 ---GAAAGGCGCGCATCGATGTTAAAGGGCAGCATTTTGAGCTGTACCGTTCGGAACG 1331
 Qy 445 GlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAla 464
 Db 1332 GCGAGGAGAGCTCCCGAGGATGCTTTTACCATCAGGAGGTGGTTCATCATTAATGGG 1391
 Qy 465 SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484
 Db 1392 ACGATGATTCATCTTCGATTGGAAGCTG-----CCCGACGCG----- 1430
 Qy 485 ***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer 504
 Db 1431 ---TCCGCCCATGTTGATATGCGCAAGCGCGGCTCAGCGCACCGCGAGAGCCGAT 1487
 Qy 505 LeuValCysValProLeuAlaArgIle 513
 Db 1488 TTGTTTTCCTGCTGGTGGTCCGCGAGTT 1514

RESULT 11

US-10-411-225-7
 ; Sequence 7, Application US/10411225
 ; Publication No. US20040261146A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mizutani, Masako

US-10-424-599-78567

Alignment Scores:

Pred. No.: 2,15e-116 Length: 3328
Score: 877.50 Matches: 188
Percent Similarity: 57.03% Conservative: 92
Best Local Similarity: 38.29% Mismatches: 183
Query Match: 36.73% Indels: 28
DB: 17 Gaps: 8

US-09-857-581B-66 (1-521) x US-10-424-599-78567 (1-3328)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
DB 176 CCACCAAGTCA---AAGGCCCTTCCATAATTGGCCACCTCCACCTTGG---TCCCCA 229
QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer***** 74
DB 230 ATTCCCCCACCAGATTTTACAAGCTCTCAACCGCCGACGAGCCATCATGCAACTTTTC 289
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuGln 94
DB 290 CTTGGCTCAGTCCCTGTGTGGCTTCCACCGCAGACCGCCAAAGAGTTTCCTTAA 349
QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
DB 350 ACCCAGAAATCAACTTCTCAACCGCCGCGCAAAACGTGCGGTAAAGGCTTAGCC 409
QY 115 TyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheVal 131
DB 410 TAGGATTCACCAAGACTTCTTTTTCGCGTTCGACCCCTTCGACCCCTACTCGAAGTTTCATG 469
QY 132 ArgLysLeuLeuMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeu 151
DB 470 AAGAAACTCTGCATTCGCGAGCTTCTCAGCGCGCGAATGATGACCACTTCCTTCCCGTG 529
QY 152 ArgThr-GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***Ly 171
DB 530 AGGTACAGACAGACCAAGAGATTCATCAGCGCGGTTCGGAAGAGAGTCGCGCGCA 599
QY 171 sProLeuAsp***ThrGluGluLeuLysTrp***AsnSerThr***SerMetMet** 191
DB 590 GGCGGTGGATTCGAGACAGAGCTCATGACACTCTCCAAACAACATCGTATCCAGATGAC 649
QY 191 *Leu-----GlyGluAlaGluGluIleArgAspIleAlaAr 203
DB 650 GCTGAGTCAGAAGACTTCTGAGACAGCAACACGAGCTGAGGAGATGAAGAGTCGTGTC 709
QY 203 gGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys** 223
DB 710 GAATATCGGAGCTCATGCGGAGTTCAAGTTTCGAGCTTCATTTGGTACTCGAAGCC 769
QY 223 *LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProVa 243
DB 770 TTTGATTTGAGGGTTCAACAGAAAATCAAGGAGACTCGGACAGAGTTTACGTTGT 829
QY 243 lValGluArgValIleLysLysArg***IleValArgArg***AsnGlyGlu** 263
DB 830 GGTGAGCGGAATCAATGAAGCAGCGTCAAGAG-----GAAAGAGGAAGAAACAAGAAC 883
QY 263 ***GluGlyGlu***SerGlyVal***LeuAspThrLeuGluPheAlaGluAspG1 283
DB 884 GGGCAGACAGCTCAGTTTAAGGATATGCTTGATGTTTATTCGACATAGCGGAGATGA 943
QY 283 uThr***GluLeuLysIleThrLys*****Ile***GlyLeuValValAsp***PheSe 303
DB 944 CAGTCTCTGAATCAATCAATCAACAAAGAAAACATTAAGCCCTTCATCATGATATATTGT 1003
QY 303 rAlaGly***AspSerThrAla*****ThrGluTyrAlaLeuAlaGluLeuIleAsnAs 323
DB 1004 TGCGGGAGCTGACAGCTGCAACCATGGAATGGGCTTATGTCAGAGTTATCAACAA 1063
QY 323 nPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***Le 343

DB 1064 TCCATATGTGTGGAGAGGCAAGGCAAGATAGATCGGTGTTGGAAAAAGTAGAAT 1123
QY 343 uValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPh 363
DB 1124 GGTAGAAGAATCAGATATTGCCAACCTTCTCTACTTTGCAAGCCATTGTTAGAGAAACACT 1183
QY 363 eArgMetHisProProLeuProValValLysArgLysCys***GluGluCys***IleAs 383
DB 1184 TAGGCTTCAACCCAGGTGCTCATTTGTTAGAGAAATCATCAAAAGTGCAGGTGTTT 1243
QY 383 nGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***As 403
DB 1244 TGGGTATGATATTCACAGAAAGACTCGATTATTGTTCATTTGTTGGCTATTGTTAGGA 1303
QY 403 p***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***Al 423
DB 1304 TCCCAATCACTGGGAGAAACCTTTTTCAGTTTAGCCAGAGAGTTTATCAGA----- 1355
QY 423 aGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheG1 443
DB 1356 -GATGGGCAA---AATCAATGATGATTTAGGGGCAACATTCATTTATTTCATTCGG 1411
QY 443 YSerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLe 463
DB 1412 GAGTGAAGAAGAACCTGCTGCTTCTCTAGCGTGCAGGTTGTGCTGTGAATCT 1471
QY 463 uAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLy 483
DB 1472 GGCTATAATTAATTCATATGTTTCCATGGAAGCTTGTGTGGCAATGCG----- 1520
QY 483 sGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHi 503
DB 1521 -----AAGTGACATGAAGAAGAAGCTGTCATCCTCTCCGAGGGCTAA 1567
QY 503 sSerLeuValCysValProLeuAlaArgIle 513
DB 1568 CCCATAATTTGTGTCCTGTTTCCAGGATT 1598

RESULT 14

US-10-424-599-120588
; Sequence 120588, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 120588
; LENGTH: 1842
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7989C.1
US-10-424-599-120588

Alignment Scores:
Pred. No.: 1,1e-115 Length: 1842
Score: 870.00 Matches: 189
Percent Similarity: 55.42% Conservative: 82
Best Local Similarity: 38.65% Mismatches: 192
Query Match: 36.42% Indels: 26
DB: 17 Gaps: 8

US-09-857-581B-66 (1-521) x US-10-424-599-120588 (1-1842)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54

Db 302 CACCGAGTCCAAATGCC---CTACCCATCATGTGACACCTCCACCTTCTT---TCTCCA 355
Qy 55 LeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer***** 74
Db 356 ACACCTCACCAAGATTTTTCACAACTCTCTCCGCTATGACCCATATACACCTTTT 415
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db 416 CTGTGTTCCAGTCCCTCGTGTGGTCTTCCACAGCAGAGCGCCCAAGAGTTCCTCAA 475
Qy 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 476 ACTCAAGAACCGCCCTTCTCCAACCGCCCGCTAACTGTGCGCTCGAACCTTAACC 535
Qy 115 Tyr---Asp*****ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
Db 536 TAGCGCTCGAAGACTTCTGTTCGACCCCTACGACCCCTATTGGAAGTTTATGAAGAA 595
Qy 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 596 CTCTGCATGTCCGAATCTCTCGGTGGCCACATGCTGGACCACTTCTTCCCGTGAGACAG 655
Qy 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 656 CAAGAGACAAATAATTCATCAACCGTGTCTCCAAAGGGTATTCTGTGTGAGCGCGTG 715
Qy 174 Asp***ThrGluLeuLeuLysTrp***AsnSerThr***SerMetMet***Leu--- 192
Db 716 GATTTGGGGAGAGTTTCATCCGCTCTCGAACATCATCGTGTGAGAAATGATCGTAGT 775
Qy 193 -----GlyGluAlaGluGluIleArgAspIleAlaArgGlu 204
Db 776 CAGACGAGTACTACTGAGCAGAGAACGAAGTTTGAAGAGATCAGGAAGCTGTGAAGAT 835
Qy 205 ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224
Db 836 GCCGAGAGCTCTCGGGAAGTTCAACATATCGGACTTCGTTCGTTCTTGAAGCGCTTT 895
Qy 225 LysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPheAspProValVal 244
Db 896 GATTTGAGGGGTTCAACAGAGGCTCGAAGATTTCGGAGCTGCTTTGACACCGTGTG 955
Qy 245 GluArgValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu***** 264
Db 956 GACAGATATAAAGCAACGTTGAAG---GAAAGAGCAAGCAAGATGAACCGTTGGA 1012
Qy 265 GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr 284
Db 1013 AAACGAGAAATTAAGGATATG---CTTCATGTTTGTGTTGACATATCTGAAGATGAGAT 1069
Qy 285 ***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAla 304
Db 1070 TCTGAATTAATTAACAAAGAAACATTAAGCCCAATATCTTGGACATATTAAATGCT 1129
Qy 305 Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro 324
Db 1130 GGGACTGACACCTCAGCTGTAAACGATGAATGGGCTATGGCAGAGTTAATCAACAATCCA 1189
Qy 325 ***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuVal 344
Db 1190 GGTGTGTGGAGAGGCAAGCAAGAAATGATGTCAGTGTGTGGAAAGAGTAGTA 1249
Qy 345 AspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArg 364
Db 1250 GAAAGATCAGATATGCGCAACTCTCTTACTTTGCAAGGCAATGTGTAGAGAAACATTAAGA 1309
Qy 365 MethisProProLeuProValLysArgLysCys***GluGluCys***IleAsnGly 384
Db 1310 CTTACCCAGCTGGTGCATGCTGTTTATAGAGATCATCTAGAAGAGCTGTGTTGTGGG 1369
Qy 385 ***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp*** 404

Db 1370 TATGATATTCCAGCAAGACTCGATATTATTGTCAATGTTTGGGCTATTGGTAGGACCCC 1429
Qy 405 LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGlu 424
Db 1430 AATCACTGGGAGAACCTCTTGTAGTTTAGGCCAGAGAGTTTGTGAAATGGG----- 1483
Qy 425 GlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySer 444
Db 1484 -----AAGAGTCAATTTGATGTAGGGGACCAACATTATCATCTACTTCCGTTCCGTAGT 1537
Qy 445 GlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAla 464
Db 1538 GGAAGAGAGCATGCTCTGGTACTTCTTTGGCATTTGCAAGTTGTGCATGTGCAATTTGGCA 1597
Qy 465 SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484
Db 1598 GTTCTAATTCAGTGTTCCTCAATGGAAGTTGACTGTGCAATGGC----- 1642
Qy 485 ***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer 504
Db 1643 -----AAGGTGAACATGGAAGAAAGGCTGGCATCACTCTTCCGAGGGCTCACCCC 1693
Qy 505 LeuValCysValProLeuAlaArgIle 513
Db 1694 ATAATTTGTGTCCTATTTCGAAGACTT 1720
RESULT 15
US-10-424-599-101968
; Sequence 101968, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 101968
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1906)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63093C.1
US-10-424-599-101968
Alignment Scores:
Pred. No.: 1,02e-111 Length: 1906
Score: 843.00 Matches: 185
Percent Similarity: 55.24% Conservative: 84
Best Local Similarity: 37.99% Mismatches: 190
Query Match: 35.29% Indels: 28
DB: 17 Gaps: 8
US-09-857-581B-66 (1-521) x US-10-424-599-101968 (1-1906)
Qy 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
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Qy 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db 254 ATACCCCAACCAAGATTTTACAGCTCTCACTCGCCATGAGCCCATCATGCAACTTTTC 313
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94


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Db 314 CTCGGCTCAGTCCCTGTGTGGTCTTCCACCGCGAAGCCGCAAAAGAGTTCCTCAAA 373
Qy 95 *****GluAlaThrSerPhe*****ThrArgPheGlnThrSerAla*****Arg*****LeuThr 114
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Qy 115 TyrAsp*****ValAla*****Pro*****GlyProTyrTrp*****PheValArgLysLeu 134
Db 434 TAC-----GTGTTTGGCCCTTACGGACCCCTCCGTGAAGTTCATCAAGAACTT 481
Qy 135 IleMetAsnAspLeu*****AsnAlaThrThrValAsn*****LeuArgProLeuArgThrGln 154
Db 482 TGCATGTCCGAACCTCTCGGTGGCGCATGTGACCAAGTTCCTCTCTGTGAGACACAA 541
Qy 155 GlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp 174
Db 542 GAGACAAAATAATTCATCAACACGCTCTCCAAAGGGTATCGTGTGTAAGCCGTGAC 601
Qy 175 ***ThrGluGluLeuLysTrp***AsnSerThr***SerMetMet***LeuGly--- 193
Db 602 TTCGGAGGAGGTTTCATGAGACTCTCCACACATCATTTTCGAGATGACCATGAACCAG 661
Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeu 206
Db 662 ACAGAGTTCGAGGACGAGAAACAGCGCCGAAAGATGAGATGCTGTGGCGGATGTCGCA 721
Qy 207 LysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysVal 226
Db 722 GAACATCATGGCAGGTTCAACGTGCGGACTTCATTTGGTCTTGAAGCCCTTTTGATTG 781
Qy 227 GlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProValValGluArg 246
Db 782 CAGGGGTTCAACAGAGGATCAGGAAACAGGAGTATCGACGCTGTCTTGGACAGA 841
Qy 247 ValIleLysLysArgArg***IleValArgArg***AsnGlyGlu*****GluGly 266
Db 842 ATCATCAAGCAGCGCTGAAGAG-----GAAAGAGGAAACCAACAGGAAATCGGTGGAACG 895
Qy 267 Glu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***Glu 286
Db 896 CGTCAGTTTAAGGATATACCTTGTGTGGATATAGGCGAAGATGACAGTCTCGAA 955
Qy 287 IleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly*** 306
Db 956 ATCAATTAACCAAGAGACATTAAGCGCTTCATCATGATATATTTGTTCGCGGACT 1015
Qy 307 AspSerThrAla*****ThrGluTyrAlaLeuAlaGluLeuIleAsnAsnPro***Val 326
Db 1016 GACACGTGAGTCAACCATGGAATGGGCTATGGCAGAGTTAATCAACAATCCATGTGTG 1075
Qy 327 Leu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGlu 346
Db 1076 TTGGAGAGGCAAGCAAGAGATAGATGTCAGTGGTTGGAAATAGTAGAATAATAGAGAA 1135
Qy 347 ValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMethHis 366
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Qy 367 ProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly***Val 386
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Qy 387 ***ProGluGlyAlaLeu*****PheAsnValTyrGlnValGly***Asp***LysTyr 406
Db 1256 ATTCAGCCAGACCCGATTTATTTGTCAATGTTTGGGCTATTTGAAGGGACCCCAATCAT 1315
Qy 407 TrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGlu 426
Db 1316 TGGGAGAACCCATTGAGTTTAGCGCGAGAGGTTTTTTTGA-----AATGGACAA 1366
Qy 427 Ala*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg 446
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Qy 467 IleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***Asp 486
Db 1484 ATTCAGTGTGTTTTCAGTGAAG-----TTTGATAATGGCAAT 1519
Qy 487 AlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuVal 506
Db 1520 AACAAAGTGGACATGGAAGAGAAGTCTGGCATCACTCTTCCGAGGGCTCACCCATAATT 1579
Qy 507 CysValProLeuAlaArgIle 513
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Search completed: April 29, 2005, 19:35:37
Job time : 913 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2005, 17:20:49 ; Search time 82 Seconds
(without alignments)
2116.443 Million cell updates/sec

Title: US-09-857-581B-66

Perfect score: 2389

Sequence: 1 MLLELALGLXVLALFXHLRP.....AHSILVCVPLARIGVASKLLS 521

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:**

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2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2256	94.4	521	15	US-10-310-154-735 Sequence 735, App
2	2250	94.2	521	16	US-10-659-755-2 Sequence 2, Appli
3	944.5	39.5	512	15	US-10-411-115-4 Sequence 4, Appli
4	940.5	39.4	506	15	US-10-411-115-2 Sequence 2, Appli
5	921.5	38.6	506	15	US-10-411-115-8 Sequence 8, Appli
6	919.5	38.5	509	15	US-10-424-599-149724 Sequence 149724,
7	891.5	37.3	509	15	US-10-424-599-221409 Sequence 221409,
8	870	36.4	510	15	US-10-424-599-263430 Sequence 263430,
9	843	35.3	502	15	US-10-424-599-244810 Sequence 244810,
10	807.5	33.8	579	16	US-10-437-963-150757 Sequence 150757,
11	761.5	31.9	518	16	US-10-437-963-123495 Sequence 123495,
12	730.5	30.6	516	16	US-10-437-963-169616 Sequence 169616,
13	717	30.0	513	15	US-10-424-599-243352 Sequence 243352,

14	701.5	29.4	509	15	US-10-424-599-258259 Sequence 258259, A
15	691.5	28.9	548	15	US-10-425-114-64368 Sequence 64368, A
16	657	27.5	540	16	US-10-437-963-140857 Sequence 140857,
17	651	27.2	509	14	US-10-097-559-11 Sequence 11, Appli
18	649.5	27.2	537	15	US-10-425-114-65085 Sequence 65085, A
19	637.5	26.7	508	17	US-10-669-962-17 Sequence 17, Appli
20	634	26.5	509	16	US-10-686-947-260 Sequence 260, App
21	633.5	26.5	503	16	US-10-686-947-198 Sequence 198, App
22	633.5	26.5	503	16	US-10-686-947-262 Sequence 262, App
23	632.5	26.5	504	16	US-10-686-947-196 Sequence 196, App
24	631	26.4	509	16	US-10-686-947-194 Sequence 194, App
25	631	26.4	537	16	US-10-437-963-148695 Sequence 148695,
26	627.5	26.3	495	14	US-10-021-425-29 Sequence 29, Appli
27	627.5	26.3	495	16	US-10-900-856-32 Sequence 32, Appli
28	627	26.2	509	16	US-10-686-947-268 Sequence 268, App
29	626	26.2	512	17	US-10-669-962-6 Sequence 6, Appli
30	625	26.2	502	10	US-09-909-566C-3 Sequence 3, Appli
31	625	26.2	502	16	US-10-759-813-3 Sequence 3, Appli
32	623.5	26.1	516	15	US-10-424-599-145449 Sequence 145449,
33	623	26.1	503	16	US-10-686-947-150 Sequence 150, App
34	623	26.1	513	17	US-10-669-962-15 Sequence 15, Appli
35	622	26.0	516	15	US-10-424-599-145460 Sequence 145460,
36	620.5	26.0	548	16	US-10-437-963-112652 Sequence 112652,
37	619	25.9	503	16	US-10-686-947-152 Sequence 152, App
38	619	25.9	503	16	US-10-686-947-192 Sequence 192, App
39	619	25.9	503	16	US-10-686-947-200 Sequence 200, App
40	618.5	25.9	496	14	US-10-097-559-40 Sequence 40, Appli
41	617.5	25.8	1933	16	US-10-437-963-106209 Sequence 106209,
42	616.5	25.8	500	14	US-10-097-559-39 Sequence 39, Appli
43	616.5	25.8	512	17	US-10-669-962-2 Sequence 2, Appli
44	610	25.5	513	15	US-10-424-599-250650 Sequence 250650,
45	609.5	25.5	506	16	US-10-437-963-112862 Sequence 112862,

ALIGNMENTS

RESULT 1

US-10-310-154-735
; Sequence 735, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.

Tue May 3 10:43:24 2005

APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 735
LENGTH: 521
TYPE: PRT
ORGANISM: Glycine max
US-10-310-154-735

Query Match 94.4%; Score 2256; DB 15; Length 521;
Best Local Similarity 86.8%; Pred. No. 6.7e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
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DB 121 MVPPFGYWKVFKLIIMNDLNATTNKLRLPTQIRKFLRMAQGAQKPLDLTEELL 180
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DB 301 XPSAGXDSAXTETWALAEILNPNXVLXXAREEYXSVVGKDLVDEVDTONLPYIRAIYK 360
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DB 361 ETRFMHPLPVVVKRCXECXINGVXPGALXFXFNWQVGDXXKYWDRPSEKRPFRFLE 420
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DB 421 TXAEGEAXXLDLRGXHFQLLPFGSGRMCPCGVXLTATSGXATLLASLIQCFLQVLGPQG 480
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DB 481 ILKXGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 2
US-10-659-755-2
Sequence 2, Application US/10659755
Publication No. US20040128711A1
GENERAL INFORMATION:

APPLICANT: DIXON, RICHARD A.
APPLICANT: LIU, CHANG-JUN
APPLICANT: DEAVOURS, BETTINA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF FLAVONOID
FILE REFERENCE: NBL:007US
CURRENT APPLICATION NUMBER: US/10/659,755
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,447
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 521
TYPE: PRT
ORGANISM: Soybean
US-10-659-755-2

Query Match 94.2%; Score 2250; DB 16; Length 521;
Best Local Similarity 86.6%; Pred. No. 3.4e-255;
Matches 451; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 1 MLELALGLXVLALFXHLRPTTAXSKALRHLNPPSPXPRLPFIHGHLLKOKLLHYAX 60
DB 1 MLELALGLLVALLFLHLRPTTAKSKALRHLNPPSPKPLPFIHGHLLKOKLLHYAL 60
QY 61 IDLSKKGHPLFSXFGSMPTVASTPELFLQXKEATSPTRFQTSAXRLTYDXXVA 120
DB 61 IDLSKKGHPLFSXFGSMPTVASTPELFLQXKEATSPTRFQTSAXRLTYDXXVA 120
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RESULT 3
US-10-411-115-4
Sequence 4, Application US/10411115
Publication No. US20040003431A1
GENERAL INFORMATION:
APPLICANT: Mizutani, Masako
APPLICANT: Kasumi, Takaaki
APPLICANT: Ayabe, Shin-ichi
APPLICANT: Akashi, Tomoyoshi
TITLE OF INVENTION: Genes Coding for Flavone Synthases
FILE REFERENCE: 001560-383
CURRENT APPLICATION NUMBER: US/10/411,115
CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US/09/672,785

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; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Torenia hybrida
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-10-411-115-4

Query Match      39.5%; Score 944.5; DB 15; Length 512;
Best Local Similarity 38.9%; Pred. No. 1.1e-101;
Matches 193; Conservative 94; Mismatches 182; Indels 27; Gaps 8;

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Db 29 PSFPGPL-SLPIIGHLHLGPR-LHHTPHEFSKYGLIQLKGLSIPCVAVSTPELAREF 86
Qy 93 LOXEATSEFTRFOTSAEXELTYDXVAXXPXGYPWVFRKLMNDLKNATTVNKLPLR 152
Db 87 LKTNB-LAFSRKSHSTAIDIVTYSFSAFSPYGYWYKFKLCTYELLGARNLGHFQPIR 145
Qy 153 TQQRKRLXMAQXAEAKPLDXTTELLKWNXTXSMXKL-----GEAEERDIARE 204
Db 146 NLEVRSLQLLWHKSFSGESVNVTDLVRLTSNVISHMMLSIKSCSEDEGDAEAARTVIRE 205
Qy 205 VLKIXGYSLTDFIXPLKXKLVGKYEKRIDDILNKPDPVVRVVKRRXIVRRRXNGEXX 264
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Db 384 VNGYKIQAKSLLFVNIWSIGNPNYWSPEFRPERFLEKRE----SIDVKGQHFELLP 439
Qy 442 FSGRXMCPGVKXATSGATLLASLIQCFDQVLGPOGQILKGDAXKVSMEERAGLTVPR 501
Db 440 FGTRGRGCPGMLLAQEVVSIIGTMVQCFD-----WKLADSGNNVDMTSGLTAPR 492
Qy 502 AHSLVCPVLARIGVAS 517
Db 493 AFDLVCRLYPRVDPAT 508

RESULT 4
US-10-411-115-2
; Sequence 2, Application US/10411115
; Publication No. US20040003431A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takeaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/10/411.115
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; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-10-411-115-2

Query Match      39.4%; Score 940.5; DB 15; Length 506;
Best Local Similarity 39.8%; Pred. No. 3.2e-101;
Matches 196; Conservative 86; Mismatches 185; Indels 25; Gaps 9;

Qy 30 RHLNPPSPXPRLPFIGHXHLKDLHYAXIDLKXKHGPLFSXXFGSMPTVAVSTPELFLP 89
Db 24 RRKTRPGPL-AUPLIGHLHLGPK-LHHTFHQFSQRYGPLIQLYLSGSPCVAVSTPELA 81
Qy 90 KLFLQXXEATSEFTRFOTSAEXELTYDXVAXXPXGYPWVFRKLMNDLKNATTVNKL 149
Db 82 REFLLKTHE-LDFSRKSHSTAIDIVTYSFSAFSPYGYWYKFKLCTYELLGARNLSHFQ 140
Qy 150 PLRTOQIRKRLXMAQXAEAKPLDXTTELLKWNXTXSMXKL-----GEAEERDI 201
Db 141 PIRALEVNSFLRILYKTEQKQSVNVTTELKLTNSVINMMLGIRCSGTEGEAEVARTV 200
Qy 202 AREVLKIXGYSLTDFIXPLKXKLVGKYEKRIDDILNKPDPVVRVVKRRXIVRRRXNG 261
Db 201 IREVTQIFGFDVSEIWFVFCNLDLQIRKSEDIRRYDALLEKIIISDRERL-RLRGGG 259
Qy 262 EXXEGEXSGVXLDTLLFEAEDETXEIKITXXIXGLVVDXFSAGXDSTAXXTEWALAEI 321
Db 260 GGGGGEVKD-FLDMLLDVMESEKSEVEFTRHLKALILDFTAGTDTTATATEWALAEI 318
Qy 322 NNPVLXXAREEYSVVGKDXLVDVDTQNLPIYRAIVKETFRRMHPPLPVVVKRCXSECK 381
Db 319 SNPNVLKKAQDEMDKVTGSQRLQESDAPNLPLYLNAIKETFRHLHPPIPLMRKSI 378
Qy 382 INGXXPEGALKXFNVMQVGDXXKYWRPSEKRPERFLETXAEGAXXLDLRGXHFOLLP 441
Db 379 VNGYTPAKTLLFVNLWSMGRNPNYWNPEFRPERFLEK-----TGSIDVKGQHFELLP 434
Qy 442 FSGRXMCPGVKXATSGATLLASLIQCFDQVLGPOGQILKGDAXKVSMEERAGLTVPR 501
Db 435 FGTRGRGCPGMLLMQELFSIIGAMVQCFDWKL--PDGV-----KSDVDMTERPGLTAPR 486
Qy 502 AHSLVCPVLARI 513
Db 487 ANDLVCOLVPRI 498

RESULT 5
US-10-411-115-8
; Sequence 8, Application US/10411115
; Publication No. US20040003431A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takeaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
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; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/10/411,115
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JF00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JF00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Perilla frutescens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-10-411-115-8

Query Match      38.6%; Score 921.5; DB 15; Length 506;
Best Local Similarity 38.9%; Pred. No. 5.6e-99;
Matches 190; Conservative 91; Mismatches 183; Indels 25; Gaps 8;

QY 33 PNPSPRLPFIQHXHLLKDKLLHYAXIDLSKXGKGLFSSXFGSMPTVASTPELPLKLF 92
DQ 27 PYPGPPF-LPTIQLHLGLPR-LHQTPHDLQRYGQPLQMLRLGSIQRCVIAASDELAKEC 84
QY 93 LQXEAATSFTRFOTSAKRLTYDXVAXXPGPYWVFKRLIMNDLXNATVXKLPLR 152
DQ 85 LKTHLV-FSRKSTAIIVTSSFAFSPGYWKFVKLLCTYELLGARNLAHQPIR 143
QY 153 TQIKRLXMAQXAAKPLDXTTELLKWNXSTXMMXL-----GEAEIRDIARE 204
DQ 144 TLEVKSLQILMRKSGESFPNTEELVKLTSNVISHMWSLIRCSSETSSEAEARTVIRE 203
QY 205 VLKIXGEYSLTDFXPLKXKLVGKYEKIDILLNKFPVVERVVKRRXIVRRXNGEXX 264
DQ 204 VTQIFGEFVDSIIWLCKNFQGIKRSEDIQRRYDALLEKIITDREK--QRRTHGGGG 261
QY 265 EGEXSGVKLDTLLEFAEDTETXIKITXXIXGLVVDXFSAGXSDTAXXTWALAEIINN 324
DQ 262 GGGAKDFLWFLDIMGSKAEVFTREHLKALILDFTAGTDTTAIVCEWATAEVINN 321
QY 325 XVLLXAREEYSVVGKDXLVDVDTQNLPIYIRAIKVTETFRMHPPPLPVVKKKCEXKING 384
DQ 322 NVLKAQEEIANIVGFDRIQLQESDAPNLPYLQALIKETFRHLPPIMLARKSISDCVIDG 381
QY 385 XVXPEGALXPNVQVGVXKDYWRDPSEKPERFLETYAEAGEAXXLDLKGXHFQLLPFGS 444
DQ 382 YMI PANTLLFVNLWSMGRNPKIWDYPTAFQPERLEK---EKAAIDVKGQHPFLLPFGT 437
QY 445 GRXKCPGVXLATSCXATLLASLIQCFDLOVLGPOGQILKXGDAKVSMEERAGLTVPEAHS 504
DQ 438 GRRCCPGMLLAIQEVIIGIMIQCFDWKL---PDG-----SGHVDMAERPGLTAPRET 489
QY 505 LVCVPLARI 513
DQ 490 LFCRVVPRV 498

RESULT 6
US-10-424-599-149724
; Sequence 149724, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
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; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 149724
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106222C.1.pap
US-10-424-599-149724

Query Match      38.5%; Score 919.5; DB 15; Length 509;
Best Local Similarity 39.8%; Pred. No. 9.6e-99;
Matches 198; Conservative 86; Mismatches 184; Indels 29; Gaps 9;

QY 29 LRHLPPPPSPXPR-LPPIGHXHLKDKLLHYAXIDLSKXGKGLFSSXFGSMPTVASTPE 87
DQ 30 LRHKPRRP-EGPRSLPPIGLHLI-SALPHQSFHALSTRYGPVAVQVFLGSPVAVVWSCPE 87
QY 88 LFKLFLQXEAATSFTRFOTSAKRLTY-DXXVAXXPGPYWVFKRLIMNDLXNATV 146
DQ 88 LAKEFLKTHE-PSFSNRFVSAAVHHLSYSGKGLFAPYGSYWFPLKICMSELLGGRTLD 146
QY 147 XLRLPTQIQRKRLXMAQXAAKPLDXTTELLKWNXSTXMMXL-----GEABEI 198
DQ 147 QFRHLREQETLRFLRLVLRKAGEAHEAVDSGELMTLTNSVISRMVLSRTCCESDGDVEHV 206
QY 199 RDIAREVLKIXGEYSLTDFXPLKXKLVGKYEKIDILLNKFPVVERVVKRRXIVRRR 258
DQ 207 RRVADTAELAGKFNLAADFVWLCKGLDLHGKIKRLVGLERFDGMDRVRVREHEERERR 266
QY 259 XNGEXXEGXSGVKLDTLLEFAEDTETXIKITXXIXGLVVDXFSAGXSDTAXXTWALA 318
DQ 267 K--ERGEGERDILLDLLEIHOESREIKLSRENVKAFILDIYMAGTDTSAITMEWALA 324
QY 319 ELINNPAVLXAREEYSVVGKDXLVDVDTQNLPIYIRAIKVTETFRMHPPPLPVVKKKCE 378
DQ 325 ELINNHHVMEKARQEDISVTGNKRLIQESDLPNLPYLOAIVKETLRHPTAPLLGRESSE 384
QY 379 ECKINGXVXPEGALXPNVQVGVXKDYWRDPSEKPERFLETYAEAGEAXXLDLKGXHFQ 438
DQ 385 SCNVCGTIDIPAKSLVFNLSMGRDPKIEWEDPLEFKPERFMN---NNEDKQIDVRGQNFQ 441
QY 439 LLPFGSGRXKCPGVXLATSCXATLLASLIQCFDLOVLGPOGQILKXGDAKVSMEERAGLT 498
DQ 442 LLPFGTGRRLCPGASLALQTVPTNVAAMLQCFEFRV-----DGTVSMEERKPA 490
QY 499 VPAHSLVCPVLARI 515
DQ 491 LPRAPHLICVVPVRMNL 507

RESULT 7
US-10-424-599-221409
; Sequence 221409, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 221409
; LENGTH: 509
```

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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(509)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41962C.1.pap
US-10-424-599-221409

Query Match      37.3%; Score 891.5; DB 15; Length 509;
Best Local Similarity 38.4%; Pred. No. 1.9e-95;
Matches 188; Conservative 92; Mismatches 183; Indels 27; Gaps 8;

Qy 35 PPSPXPLPFIIGHXHLKDLXLLHYAXIDLKSKHGFLFSXXFGSMPTVASTPELFLQ 94
Db 30 PPSP-KALPIIIGHHLV-SPIPHQDFYKLSRHHGPIHQLFLGSPVPCVASTAEAKFLK 87

Qy 95 XEATSEFTRFQTSAXRLTYDXXVAXXPXGPYKXFKLVKRLIMNDLXNATTVNXLRLP 151
Db 88 THEINFNSRPGQNVAVKGLAYDSQDFLFAFAPFGPYKFKMKKLCWSELSSGRNMDQLPV 147

Qy 152 RTQIRKXLRMAQXAEAKPLDXTTEELLKXNXTXMMXL-----GEABEIRDIAR 203
Db 148 RXQETKRFISVRKGVAGEAVDFGDELMTLSNNIVSRMTLSQKTSENDNQAEEMKKLVS 207

Qy 204 EVLKIXGEYSITDFIXPLKXKLVKGYEKRIIDILNKFPVVERVVKRRXIVRRXNGEX 263
Db 208 NIAELMGKFNVSDFIWLKPPDLQGFNKKIKETRDREDFVVDGIIKQRE--ERRKNKET 265

Qy 264 XEKGSGVKLDTLLEFADETXEIKITKXXIXGLVVDXFSAGXDSAXXTWALAEIINN 323
Db 266 GTARQKQMDLVLLDIGDSDSEIKLTKENIKAFIMDFIVAGTDTSAATMEWMAELINN 325

Qy 324 PXVLXXAREEYXSVGVKDXLVDVDTQNLPIYIRAIKVTETFMHPPLPVKXCKEEXCIN 383
Db 326 PYVLEKARQEDAVGVGRMVEESDIANLPYLQAIVRRETLRHPGGVLVRESSKSAVVC 385

Qy 384 GXVPEGALXXFNVMQVQXKXKWDPRSEXPXPERFLETXAEGEAXXLDLKGXHFQLLPFG 443
Db 386 GYDIPAKTRLFVNVWAIGRDPNHWKPEFPERFIR---DQO-NQLDVRGQHYHFPFG 441

Qy 444 SGRXWCPGVKXATSLASLQCPDLQVLGPOGQILKXGDAKXVMEERAGLTVPRAH 503
Db 442 SGRRTCPGASLAWQVVPVNLAIQCFOWKLVGGNG-----KVDMEKSGITLPRAN 493

Qy 504 SLVCVPLARI 513
Db 494 PIICVPVPRI 503

RESULT 8
US-10-424-599-263430
; Sequence 263430, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 263430
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7989C.1.pap
US-10-424-599-263430
```

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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(509)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41962C.1.pap
US-10-424-599-221409

Query Match      36.4%; Score 870; DB 15; Length 510;
Best Local Similarity 38.7%; Pred. No. 6.4e-93;
Matches 189; Conservative 82; Mismatches 192; Indels 26; Gaps 8;

Qy 35 PPSPXPLPFIIGHXHLKDLXLLHYAXIDLKSKHGFLFSXXFGSMPTVASTPELFLQ 94
Db 32 PPSPMP-LPIIIGHHLV-SPTPHQDFYKLSRHHGPIIHLFLGSPVPCVASTAEAKFLK 89

Qy 95 XEATSEFTRFQTSAXRLTYDXXVAXXPXGPYKXFKLVKRLIMNDLXNATTVNXLRLP 153
Db 90 THEPAPSNRRPANTVAVETLIYASEDFLFAFAPFGPYKFKMKKLCWSELSSGRNMDQLPV 149

Qy 154 QOIRKXLRMAQXAEAKPLDXTTEELLKXNXTXMMXL-----GEABEIRDIARE 204
Db 150 QETKFKIRVLQKIGSCEAVDFGGEFTLSNNIVSRMIVSQTSTTDENEVEEMKLVKD 209

Qy 205 VLKIXGEYSITDFIXPLKXKLVKGYEKRIIDILNKFPVVERVVKRRXIVRRXNGEX 264
Db 210 AELSGKFNISDFVSLKRFDLQGFNKKIKETRDREDFVVDGIIKQRE--ERRKNKET 268

Qy 265 EGEKSGVKLDTLLEFADETXEIKITKXXIXGLVVDXFSAGXDSAXXTWALAEIINN 324
Db 269 KRFEKDM-LVLPDISDESEIKLKENIKANILDLIAGTDSAVTMEWMAELINN 327

Qy 325 XVLXXAREEYXSVGVKDXLVDVDTQNLPIYIRAIKVTETFMHPPLPVKXCKEEXCIN 384
Db 328 GVLEKARQEDAVGVGRMVEESDIANLPYLQAIVRRETLRHPGGVLVRESSKSAVVC 387

Qy 385 XVPPEGALXXFNVMQVQXKXKWDPRSEXPXPERFLETXAEGEAXXLDLKGXHFQLLPFG 444
Db 388 YDIPAKTRLFVNVWAIGRDPNHWKPEFPERFIR---KSQLDVRGQHYHLLPFG 443

Qy 445 GRXWCPGVKXATSLASLQCPDLQVLGPOGQILKXGDAKXVMEERAGLTVPRAHS 504
Db 444 GRACPTSLALQVHVHNLAVLQCFOWKLVGGNG-----KVNMEKAGITLPRAP 495

Qy 505 LVCVPLARI 513
Db 496 IICVPIRL 504

RESULT 9
US-10-424-599-244810
; Sequence 244810, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 244810
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63093C.1.pap
US-10-424-599-244810

Query Match      35.3%; Score 843; DB 15; Length 502;
Best Local Similarity 38.0%; Pred. No. 9.4e-90;
Matches 185; Conservative 84; Mismatches 190; Indels 28; Gaps 8;

Qy 35 PPSPXPLPFIIGHXHLKDLXLLHYAXIDLKSKHGFLFSXXFGSMPTVASTPELFLQ 94
Db 30 PPSP-KGLPIIIGHHLV-SPIPHQDFYKLSRHHGPIHQLFLGSPVPCVASTAEAKFLK 87
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Db 188 NSIMRWASALPGEMAEARCAKQVAVELVGAFAEDFVAVCRGWDLQGIQRRNEVHAR 247
Qy 240 FDPVVERVVKRRXITVRRRXNGEXXGKXGVLDTLLLEFAEDTETXETIKTKXIXGLV 299
Db 248 FDALLEITIEAKEE-ARRSLRGRRESSKDLMLMDAAEDDTAEVKLTEDNIKAFVL 306
Qy 300 DXFSAGXSTAXXTWALAEALNNPXVLXAXAREEYXSVGKDXLVDVDTONLPIRAIV 359
Db 307 DIFTAGSDTTATTVEMLAELVNHPECMAKRLGELDAVVGSRSLVGEQDVARLPYLA 366
Qy 360 KETFRMHPLPVKRRKCEEXKXGKXVPEGALXXFNWOGXDKKYWDPRSEKRPERFL 419
Db 367 KETLRLPVPAQVTVPEVQVRGTYTPTDQVFFNIFSGRDTYWDQDLPFRPDRFL 426
Qy 420 ETXAEGEAXLDRGHFQLLPFGSGRXMCPGVXLATSGXATLLASLQCFDLQVLGPQG 479
Db 427 ---PDGAGATVDPKQHQHPLMPFGSGRRACPGMLAMQAVPAFLAALVQCDFW--APPS 481
Qy 480 QILKXDAKVSMEERAGLTVFRAHSLVCUPLARI 513
Db 482 QPL-----PLDMEEAAGLVLSARKHPHLLLLPTPRI 510

RESULT 12

US-10-437-963-169616
; Sequence 169616, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169616
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68019C.1.pap
US-10-437-963-169616

Query Match 30.6%; Score 730.5; DB 16; Length 516;
Best Local Similarity 35.3%; Pred. No. 1.7e-76;
Matches 169; Conservative 79; Mismatches 204; Indels 27; Gaps 11;
Qy 35 PPSXPRLPFTGHXHLKDLHYAXIDLSKKGHGLFSSXFGSMPTVVASTPELFLQ 94
Db 44 PPSPA-SLPVIGHLLHLLAPP-VHRTFHELAARGLPLMHVRLGTHCVASSAEVAELIR 101
Qy 95 XEATSFYTRQTSAXRXLTYDXX-VAXXPXGPYKXFKRLIMNDLXNATVNXLRPLRT 153
Db 102 SHEA-KISERPLTAVARQFAYESAGFAPYSPHWRFMKLCMSSELLGRTVEQLRPVRR 160
Qy 154 QOIRKXLRMAQXABAXKPLDXTBELLKXNXTXSMXILGE-----AEEIRDIAREVLKI 208
Db 161 AGLVSLRHVLISQPEA-EAVDUTRELIRMSNTSIIRMAASTVPSSVTEAQELVKVVAEL 219
Qy 209 XGEYSLDTFPLKXKLVKYEKRIIDDILNKFPDPVVERVVKRRXIVRRRXNGEXXGEX 268
Db 220 VGAFNADDYIALCRGWDLQGLGRRRAADVHKRFDALLEEMIRKHEE-ARMKKTDTDVG-- 276
Qy 269 SGVXLDTLLLEFAEDTETXETIKTKXIXGLVVDXFPAGKXSTAXXTWALAEALNNPXVLX 328
Db 277 SKDLLDILLDKAEDGAAEVLKTRDNIKAFIIDVVVTAGSDTSAAMVEMVMAELMNHPEALR 336

Qy 329 XAREEXYSVVGKDXLVDVDTQNLPIYIRAIVKETFRMHPPLPVVKRCKEBCXINGXYXP 388
Db 337 KVREEIEAVVGRDRIRAGEGDLPLPYLQAAYKETLRLRPAAPIAHQSTEBEIQIRGFRVP 396
Qy 389 EGALXXFNWOGXDKKYWDPRSEKRPERFLETXAEGEAXXLDLGRGHFOLLPGSGRXM 448
Db 397 AQTAVFNNVAIGRDPAYWEPLFRPERFL---AGGGEGVEPRGQHFQMPFGSGRRG 453
Qy 449 CPGVXLATSGXATLLASLQCFDLQVLGPQOQILKXDAK-VSMEEERAGLTVFRAHSLV 506
Db 454 CPGMLALOSVPAVVAALLQCFDQCM-----DNKLIDMEADGLVCARKHLL 502

RESULT 13

US-10-424-599-243352
; Sequence 243352, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 243352
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_61775C.1.pap
US-10-424-599-243352

Query Match 30.0%; Score 717; DB 15; Length 513;
Best Local Similarity 34.3%; Pred. No. 6.3e-75;
Matches 170; Conservative 78; Mismatches 224; Indels 24; Gaps 8;
Qy 27 KALRHLPNPPSPXPRLPFIHGHXHLKDLHYAXIDLSKKGHGLFSSXFGSMPTVASTP 86
Db 26 KKPQRLRPPGPPIISIPLLGHAPYLR-SLLHQALYKLSLRYGPIHVMIGSKHVVVASSA 84
Qy 87 ELFKLQXXEATSFYTRQTSAXRXLTYDXX-VAXXPXGPYKXFKRLIMNDLXNATV 145
Db 85 ETAKQILKTSE-EAFNRPMLIAESLTYGAADYFFPYGYWRFKLLCMTTELLSGKTL 143
Qy 146 NXLRPLRTOQIRKXLRMAQ-XABAXKPLDXTBELLKXNXTXSMXILG-----BAE 196
Db 144 EHFVRIRESEVEAFKRMWEISGNGYEVVMRKELITHTNNTIIRMIWKKKSAENDEVA 203
Qy 197 EIRDIAREVLKIXGEYSLTDFIXPLKXKLVKYEKRIIDDILNKFPDPVVERVVKRRXIVR 256
Db 204 RLKRVVREVGELLGAFNLGDIVGFMRPLDLOGFGKQNMETHHKKVDAMMEKVLREHEARA 263
Qy 257 RXNGEXXGEXSGVXLDTLLLEFAEDTETXETIKTKXIXGLVVDXFPAGKXSTAXXTWA 316
Db 264 K-----EADSDRKKDLFDILNLTADGADNKLITRESAKAFALDNFINGTPASVLBS 319
Qy 317 LAELINNPVXLXAREEXYSVVGKDXLVDVDTQNLPIYIRAIVKETFRMHPPLPVVKRKC 376
Db 320 LAELVRNPHVFKAREEIESVVGKRLVKESDIPNLVYLQAVLKETLRLHPTPIFAREA 379
Qy 377 XEECXINGXVPEGALXXFNWOGXDKKYWDPRSEKRPERFLETXAEGEAXXLDLGRXH 436
Db 380 MRTQVEGYDIPENSTILISTWAIGRDPNWDALYKPERFLFSDDPGKS-KIDVRGQY 438
Qy 437 FOLLPGSGRXMCPGVXLATSGXATLLASLQCFDLQVLGPQOQILKXDAKVSMEERAG 496
Db 439 YOLLPGSGRRSCPGASLALLVMQATLASLQCFDWIV-----NDGNHHHVDMSBGR 491

Qy 497 LTVFRAHSLVVCVPLAR 512
Db 492 VTVFLAKLCKPVP 507

RESULT 14

US-10-424-599-258259
; Sequence 258259, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 258259

; LENGTH: 509

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_75231C.1.pep

US-10-424-599-258259

Query Match 29.4%; Score 701.5; DB 15; Length 509;

Best Local Similarity 32.6%; Pred. No. 4.2e-73;

Matches 169; Conservative 82; Mismatches 227; Indels 41; Gaps 12;

Qy 11 VLALFXHLRPTPPXAXSKALRHLNPPSPXPLPFIGHXHLKDKLLHYAXIDLSKKHGL 70

Db 5 IVFLFLLLSLSSSSNNLSQLPPSP-PSIPLLGLHLHTPS-LYKSLYTLSSKRGPL 62

Qy 71 FSXXFGS-----MPTVVASPELFFK---LFLQXKEATSPFTR--FOTSAXRXLTYDXV 119

Db 63 LLLRLGFSRRLLLVSSNAVATVFKTHDLAFSSRPAPAFARLPFGTSG-----F 113

Qy 120 AXXPXGYPWFVRKLIWMDLNATVXKLRLPTQQIRKXLRXMAQXAEAKPLDXTEEL 179

Db 114 VTAPYGPYWRPMKKLCVTELLSTQLRERSIRREEILRSIKRVIDNARETVADLGSF 173

Qy 180 LKWN-----STXSMXKLGAEERDAREVLKIXGEVSLTDFIXPLKXKLVGKYEK 231

Db 174 TKFTNNVTCTAMTSCAEKCEDAERIRKLVKESFELAAKLCFGDVLGPFKLSFWYVGK 233

Qy 232 RIDDILNKFDPVVERVIKRRXIVRRRXNGEXXEGEXSGVKLDTLLEFAEDETXEIKITK 291

Db 234 KAIDMSTRYDELLLEVLKEHEHKLSTRANDOSERD---LMDILLDVYHDAHAEFKITM 289

Qy 292 XXIXGLVVDXPSAGSDTAXTEWALAEILNPPXVXXAREEYXSVVGKDXLDEVDTON 351

Db 290 AHIAKAFMDLFIAGTHTSABATOWAMAEILLNHPAFQKVRKEITELVTGNVRLVDESITN 349

Qy 352 LPYIRATVKTFRMHPLPVVKKCXEECKINGVXPEGALXXFNWQVGDXXKYYDRPS 411

Db 350 LPYLOAVVKTETRLYPAPITTREROCHKINSFVPPKTAVALNIAIMRDPDSWDNPN 409

Qy 412 EXPRPERLETXAEGEAXKLDLRGHFQLLPFGSGRXXMCPGVXLTATSGXATLLASLIQCFD 471

Db 410 EFCFERFLO-EQDHEDLSDDGKMKFNFPVFGGGRRCGPTALAFSLMNTAVAMVQCDF 468

Qy 472 LQVLGPOGQILKGXDAKVSMEERAGLTVPRAHSLVVCVPL 510

Db 469 WKI-GKDG---KG--EKVDMESGSGMSLSMVHPLICVPV 501

RESULT 15

US-10-425-114-64368

; Sequence 64368, Application US/10425114

; Publication No. US20040034888A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 64368

; LENGTH: 548

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3689-223-H4_FLI.pep

US-10-425-114-64368

Query Match 28.9%; Score 691.5; DB 15; Length 548;

Best Local Similarity 34.9%; Pred. No. 6.9e-72;

Matches 177; Conservative 77; Mismatches 208; Indels 45; Gaps 14;

Qy 26 SKALRHLNPPSPXPLPFIGHXHLKDKLLHYAXIDLSKKHGLPSXXFGSMPTVYAST 85

Db 55 ARSTRKYRLPPGPRP-WPVIGNLNLI-GPLPHSHVHLSKRYGLPLMSLRFSGFPVVYASS 112

Qy 86 PELFKLFLQXKEATSPFTRPOTSAXRXLTYD-XKVAAXXPXGYPWYXFKVRLIMMDLNATT 144

Db 113 VDTARLLIKTHD-LAFIDRPQTAAGRYTYNCAGLFPQPYGAYWQARRLCOAELFSARR 171

Qy 145 VNXLRPLRTOQIRKXLRXMAQXAE---XKPLDXTTEELKWNXNYSXMMKLG----- 194

Db 172 LMSLEHVRSDVRAMLSDLRASSAPAGGHDAVTLREHLYMWNLSVVSRMLLKKYVVEG 231

Qy 195 -----AEIRDITAREVLKIXGEVSLTDFIXPLKXKLVGKYEKRIIDILNKFDPVVERVI 248

Db 232 SSSPAPTEEPFRWLIDHEFFLNGVLNVADMLPWLSPDPOQGYVRMRKRSACKMLDRFLEHV 291

Qy 249 KRRXIVRRRXNGEXXEGEXSGVKLDTLLEFAEDET-XEIKITKXIXGLVVDXFSAGXD 307

Db 292 DEHNE--RRRREGEDFVMD---MMDVLELADDPQLEVPITRDNVKGFPTLDMGGGTD 346

Qy 308 STAXXTWALAEILNPPXVXXAREEYXSVVGKDXLDEVDTONLPYIRATVKTFRMH 367

Db 347 TSAVTVEWAMSELLRNPEVLAKATEELDRVYGRDLVAEGDIPSLPYLDAVVKETLRLHP 406

Qy 368 PLPVV-KRKXCRCXINGVXPEGALXXFNWQVGDXXKYWDRPSRXPRLERLETXAEGE 426

Db 407 VAPLLTFLRCREDVSGGYDIPAGARVFNVAIGRDPVAVEAPLEFRPRF-----A 459

Qy 427 AXKLDLRGHFQLLPFGSGRXXMCPGVXLTATSGXATLLASLIQCFDQLVLGPOGQILKGXD 486

Db 460 GSSVDVKGQHFELLFPFGSGRXXMCPGMGLALRMVPTILGNLLHAFANL--PDGVAAB--- 514

Qy 487 AKYSMEERAGLTVPRAHSLVVCVPLARI 513

Db 515 -ELGMEETFLGTVPR-----LVPLQAV 535

Search completed: April 29, 2005, 17:34:24

Job time : 83 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2005, 17:31:50 ; Search time 268 Seconds

(without alignments)
3180.971 Million cell updates/sec

Title: US-09-857-581B-66

Perfect score: 2389

Sequence: 1 MLEELALGLXVLAFLXHLRP.....AHSLVCVPLARIGVASKLS 521.

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool_h/US09857581/runat_29042005_104822_20983/app_query.fasta_1.711
-DB=Issued_Patents_NA -QWMT=fascap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09857581 @CGN 1 1 69 @runat_29042005_104822_20983 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2250	94.2	1824	3	US-08-948-564-13
2	944.5	39.5	1730	4	US-09-672-785-3
3	943.5	39.5	1724	4	US-09-672-785-1
4	921.5	38.6	1770	4	US-09-672-785-7
5	637.5	26.7	1660	4	US-09-142-108C-16
6	629	26.3	1488	4	US-09-689-783A-1
7	626	26.2	1711	4	US-09-142-108C-5
8	625	26.2	1781	3	US-09-499-302A-1
9	623	26.1	1748	4	US-09-142-108C-14
10	618.5	25.9	1762	3	US-08-881-784-5
11	618.5	25.9	1762	3	US-09-292-768-1
12	618.5	25.9	1762	3	US-09-292-768-65

13	618	25.9	1806	3	US-09-351-229-3
14	616.5	25.8	1665	3	US-08-881-784-8
15	616.5	25.8	1665	3	US-09-292-768-3
16	616.5	25.8	1665	3	US-09-292-768-67
17	616.5	25.8	1789	4	US-09-142-108C-1
18	615.5	25.8	1665	3	US-09-292-768-69
19	613.5	25.7	1762	3	US-09-292-768-63
20	606.5	25.4	1762	3	US-09-172-339-5
21	600.5	25.1	1515	3	US-09-292-768-5
22	593	24.8	1815	4	US-09-142-108C-18
23	590.5	24.7	1737	4	US-09-142-108C-3
24	590	24.7	1824	4	US-09-142-108C-20
25	583	24.4	1657	3	US-08-948-564-11
26	578.5	24.2	1722	3	US-09-033-055A-1
27	574	24.0	1757	1	US-08-313-075A-49
28	574	24.0	1757	4	US-09-142-108C-26
29	571.5	23.9	2174	3	US-08-606-505B-63
30	571.5	23.9	2174	3	US-09-616-990-63
31	567	23.7	1667	4	US-09-142-108C-22
32	566.5	23.7	1665	1	US-08-313-075A-29
33	565.5	23.7	1893	1	US-08-532-065B-1
34	564.5	23.6	1927	3	US-08-606-505B-64
35	564.5	23.6	1927	3	US-09-616-990-64
36	563.5	23.6	1812	1	US-08-313-075A-37
37	563.5	23.6	1824	3	US-08-606-505B-1
38	563.5	23.6	1824	3	US-09-616-990-1
39	559.5	23.4	2013	3	US-09-615-192A-404
40	557.5	23.3	1634	3	US-09-136-420A-2
41	556.5	23.3	1737	3	US-09-136-420A-1
42	556.5	23.3	1838	2	US-09-091-432-1
43	556.5	23.3	1838	4	US-09-387-663-1
44	556.5	23.3	1838	4	US-09-214-139B-2
45	555.5	23.3	1691	3	US-08-948-564-3

ALIGNMENTS

RESULT 1

US-08-948-564-13
; Sequence 13, Application US/08948564
; Patent No. 6121512

GENERAL INFORMATION:

; APPLICANT: Siminsky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

Sequence 3, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 67, Appli
Sequence 1, Appli
Sequence 69, Appli
Sequence 63, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 18, Appli
Sequence 3, Appli
Sequence 20, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 49, Appli
Sequence 26, Appli
Sequence 63, Appli
Sequence 22, Appli
Sequence 29, Appli
Sequence 1, Appli
Sequence 64, Appli
Sequence 64, Appli
Sequence 37, Appli
Sequence 1, Appli
Sequence 404, App
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli

; LENGTH: 1824 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 54..1616
 US-08-948-564-13

Alignment Scores:
 Pred. No.: 1,75e-301 Length: 1824
 Score: 2250.00 Matches: 451
 Percent Similarity: 86.56% Conservative: 0
 Best Local Similarity: 86.56% Mismatches: 70
 Query Match: 94.18% Indels: 0
 DB: 3 Gaps: 0

US-09-857-581B-66 (1-521) x US-08-948-564-13 (1-1824)

Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
 Db 54 ATGTTGCTTGAACATGCACCTTGGTTATTTGGTCTCTGTTCTGCACTTGGCTCCC 113
 Qy 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
 Db 114 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCAAACCCACCAGCCCAAGCCT 173
 Qy 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
 Db 174 CGTCTCCCTTATAGGACACCTTCACTCTTAAAGACAAACTTCTCCACTAGCCACTC 233
 Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 Db 234 ATCCACCTCTCAAAAAACATGGTCCCTTATCTCTCTACTTCTGCTCCATGCCAAC 293
 Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
 Db 294 GTTGTTCCTTCCACACAGAAATGTTCAAGCTCTTCTCCAAACGACAGGCACTTCC 353
 Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
 Db 354 TTCAACCAAGTTCCAAACTCAGCCATAGAGCGCTCACCTATGATAGTCACTAGTGCC 413
 Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu*** 140
 Db 414 ATGGTTCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC 473
 Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
 Db 474 AACGCCACCACTGTAAACAAGTTGAGGCCCTTTGGGACCCCAACAGACCCCGAAGTTCCTT 533
 Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
 Db 534 AGGTTATGGCCCAAGCGCAGAGCCACAGAGCCCTTGACCTTGACCCGAGGAGCTTCTG 593
 Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
 Db 594 AAATGGACCAACACACCATCTCCATGATGATGCTCGCGAGCGCTGAGGAGATCAGAGAC 653
 Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
 Db 654 ATCGCTCGCAGGTTCTTAAGATCTTTGGCAATACAGCTCTCACTGATCTCATCTGGCCA 713
 Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
 Db 714 TTGAAGCATCTCAAGGTTGGAAGATATGAGAAGAGGATCAGACATCTTTGAACAAGTTC 773
 Qy 241 AspProValGluArgValIleLysLysArg***IleValArgArgArg***Asn 260
 Db 774 GACCTCTCGTTGAAGGGGTCATCAAGAAGCGCGTGAGATCGTGAGGAGAGAAAGAC 833
 Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280

Db 834 GGAGAGTTGTTGAGGTTGAGGTCAGCGGGTTTTCTTGACACCTTCTGTAATTCGCT 893
 Qy 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
 Db 894 GAGGATGAGACCATGGAGATCAAAATCACCAGGACCACATCGAGGGTCTTTGTTGTGAC 953
 Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
 Db 954 TTTTCTTCGGCAGAAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTTGGCAGAACTC 1013
 Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
 Db 1014 ATCAACATCTTAAGGTGTTGAAAGGCTCTGAGAGAGTCTACAGTGTGTGGGAAG 1073
 Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
 Db 1074 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCTTACATTAGAGCAATCGTGAAG 1133
 Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
 Db 1134 GAGACATTCGCGATGACCCGCCACTCCCAAGTGGTCAAAAGAAAGTGCACAGAGAGTGT 1193
 Qy 381 ***IleAsnGly***Val***ProGluGlyValLeu*****PheAsnValTyrGlnVal 400
 Db 1194 GAGATTAAATGATATGTGATCCAGAGGAGCAATGATCTCTTCAATGTATGGCAAGTA 1253
 Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
 Db 1254 GGAAGAGACCCCAATACTGGGACAGACCATCGAGTTCGGTCTCGAGAGGTTCTTAGAG 1313
 Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
 Db 1314 ACAGGGCTGGAAGGGAAGCAGCGGCTTGTGATCTTAGGGGCAACATTTTCAACTTCTC 1373
 Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
 Db 1374 CCATTTGGGTCTGGGAGGAGATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1433
 Qy 461 ThrLeuLeuAlaSerLeuLeuGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
 Db 1434 ACATCTTCTGCACTCTTATTCACTGCTTCGACTTCAAGTGTGGGTCCACAGGACAG 1493
 Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
 Db 1494 ATATTGAAGGGTGGTACGCCAAAGTTAGCATGGAAGAGAGACCGGCTCTCACTGTTC 1553
 Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
 Db 1554 AGGCGACATAGTCTTGTCTGTGTTCCTTGTCCACTTGCAGAGATCGGCGTTGCACTAACTCCTT 1613
 Qy 521 Ser 521
 Db 1614 TCT 1616

RESULT 2

US-09-672-785-3
 ; Sequence 3, Application US/09672785
 ; Patent No. 6596927
 ; GENERAL INFORMATION:
 ; APPLICANT: Mizutani, Masako
 ; APPLICANT: Kasumi, Takaaki
 ; APPLICANT: Ayabe, Shin-ichi
 ; APPLICANT: Akashi, Tomoyoshi
 ; TITLE OF INVENTION: Genes Coding for Flavone Synthases
 ; FILE REFERENCE: 001560-383
 ; CURRENT APPLICATION NUMBER: US/09/672, 785
 ; CURRENT FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/04379
 ; PRIOR FILING DATE: 2000-01-30
 ; PRIOR APPLICATION NUMBER: PCT/JP00/00490
 ; PRIOR FILING DATE: 1999-01-28
 ; PRIOR APPLICATION NUMBER: JP 11-205229

; PRIOR FILING DATE: 1999-01-19
 ; PRIOR APPLICATION NUMBER: JP 11-22427
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.0.
 ; SEQ ID NO 3
 ; LENGTH: 1730
 ; TYPE: DNA
 ; ORGANISM: Torenia hybrida
 ; FEATURE:
 ; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
 ; OTHER INFORMATION: activity to directly convert flavanone to flavone
 US-09-672-785-3

Alignment Scores:

Pred. No.: 2, 2e-120 Length: 1730
 Score: 244.50 Matches: 198
 Percent Similarity: 57.56% Conservative: 95
 Best Local Similarity: 38.90% Mismatches: 189
 Query Match: 39.54% Indels: 28
 DB: 4 Gaps: 8

US-09-857-581B-66 (1-521) x US-09-672-785-3 (1-1730)

Qy 20 ProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProSerPro*** 39
 Db 103 CCACCACCTTCTCTCTCTCTCTCGCGCGA-AGGGAGCACCGTCTCGCGCGGTCTCTC 161
 Qy 40 ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla 59
 Db 162 ---TCCCTTACCATAATTTGGCCACCTCCACCTCTCTCGGCCCAAGA---CTCCACACACG 215
 Qy 60 ***IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetPro 79
 Db 216 TTCATGAATTTCTACTCAATATACGGCCCATTTGATCCAGCTCAAGCTCGGCTCGATCCG 275
 Qy 80 ThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThr 99
 Db 276 TGGTGTGGTCTCGACGCCGCGAGCTCGGAGAGATTCTTAAGACGAACGAG---CTC 332
 Qy 100 SerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****Val 119
 Db 333 CGGTCTCTCTCGCAAGCACTCTACGCGCCATAGACATCGTCACCTACGACTCGTCTCTT 392
 Qy 120 Ala*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu 139
 Db 393 GCTTCTCTCTCGTACGGACCTTACTGGAAGTACATCAGAAACTGTGTACTACGAGCTG 452
 Qy 140 ***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys*** 159
 Db 453 CTCGGAGCGGAACCTCGGACACTTTTCAGCCCATAGGAATCTCGAGGTCTGCTCTT 512
 Qy 160 LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 179
 Db 513 CTGCAGCTTCTGATGTCACAGAGCTTTAAGGGCGAGAGTGTGAATGTGCACAGACGAGCTG 572
 Qy 180 LeuLysTrp***AsnSerThr***SerMetMet***Leu----- 192
 Db 573 GTGAGGTGACGAGCAATGTGATATCCACCATGATGCTGACATAGGTGCTCGGAAGAT 632
 Qy 193 ---GlyGluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGlu 211
 Db 633 GAAGCGATGCTGAGCGCGGACGACATGATACGCGAGGTGACGAGATATTGGGGA 692
 Qy 212 TyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGlyLys 231
 Db 693 TTTCATGTTACGACATAATATGTTTTCAGAAATTCGATCTCGCGGGGATAAAGAG 752
 Qy 232 ArgIleAspAspIleLeuAsnLysPheAspProValGluArgValIleLysLysArg 251
 Db 753 AGTCAGAGGATATTCAGAGAGGATGATGCTTTGCTCGAAGAGATATTAGTAGAGA 812
 Qy 252 Arg***IleValArgArg***AsnGlyGlu*****GluGly-----Glu*** 268

Db 813 GAGAGA-----TCGAGGAGGCAAAATCGTATAAGCATGCTGCGGTAAACAATGAGGAG 866
 Qy 269 SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLys 288
 Db 867 GCCAAGGATTTCTGTATATGTTGTTGATGTGAGAGTGGGACACGAGGAGTCAAA 926
 Qy 289 IleThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSer 308
 Db 927 TTCTACTAGAGCATCTCAAGGCTTTGATCTGTGATTTCTTCACGGCCGTTACGACACA 986
 Qy 309 ThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*** 328
 Db 987 ACAGCCATAGCACCGAGTGGGCCATCGCGAGCTCATCAACAACCCGACGCTCTTGAAG 1046
 Qy 329 ***AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAsp 348
 Db 1047 AAGGCCCAAGAAGAAATATCCCGGATCATCCGAACCAAGCGGATCGTACAAGAATCCGAC 1106
 Qy 349 ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProPro 368
 Db 1107 GCCCCAGACCTTACCTTACCTCCAGGCCATCATCAAGGAGAGCTTCCGGCTCCACCACG 1166
 Qy 369 LeuProValValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro 388
 Db 1167 ATCCCGATGCTCTCGGTAGTCCACCTCCGATTGCACGGTCAACGGCTACAAAATCCAA 1226
 Qy 389 GluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAsp 408
 Db 1227 GCCAAGACCTCTTGTTCGTGAACATATGTTCCATCGTCCGATCGAAACCCCTAATTACTGGAA 1286
 Qy 409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428
 Db 1287 AGCCTATGAGTTTCAGCGCCGAGCGGTTCTTGAGAGGAGCGCGAG----- 1334
 Qy 429 ***LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448
 Db 1335 TCATCGACGCTCAAGGCCAGCACCTTTGAGCTCTTGTGAGCGCGCGCGAGGGGC 1394
 Qy 449 CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468
 Db 1395 TGTCCCGTATGTTGCTGGCTATACAAGAGGTGTCAGCATCATTTGGAGCATGTTTCAG 1454
 Qy 469 CysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLys 488
 Db 1455 TGCTTCGAC-----TGGAAATTGGCAGATGTTTCGGGCAATAT 1493
 Qy 489 ValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysVal 508
 Db 1494 GTGGACATGACCGAAGCGTCTGGATTGACCGCTCCGAGAGCGTTTCGATCTGTTTCCGG 1553
 Qy 509 ProLeuAlaArgIleGlyValAlaSer 517
 Db 1554 TTGTATCCAGGGTTGACCGGCCACA 1580

RESULT 3

US-09-672-785-1
 ; Sequence 1, Application US/09672785
 ; Patent NO. 6596927
 ; GENERAL INFORMATION:
 ; APPLICANT: Mizutani, Masaaki
 ; APPLICANT: Kasumi, Takaaki
 ; APPLICANT: Ayabe, Shin-ichi
 ; APPLICANT: Akashi, Tomoyoshi
 ; TITLE OF INVENTION: Genes Coding for Flavone Synthases
 ; FILE REFERENCE: 001560-383
 ; CURRENT APPLICATION NUMBER: US/09/672,785
 ; CURRENT FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/04379
 ; PRIOR FILING DATE: 2000-01-30
 ; PRIOR APPLICATION NUMBER: PCT/JP00/00490
 ; PRIOR FILING DATE: 1999-01-28
 ; PRIOR APPLICATION NUMBER: JP 11-205229

```
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; activity to directly convert flavanone to flavone
US-09-672-785-1

Alignment Scores:
Pred. No.: 3,01e-120 Length: 1724
Score: 943.50 Matches: 198
Percent Similarity: 57.31% Conservative: 88
Best Local Similarity: 39.68% Mismatches: 179
Query Match: 39.49% Indels: 34
DB: 4 Gaps: 9

US-09-857-581B-66 (1-521) x US-09-672-785-1 (1-1724)

Qy 33 ProAsnProSerPro***Pro-Arg-----LeuPr 43
Db 87 CCTCACCTCTTAACCGCGACCGCGCGAGACCGCGCGCGCCCGCCATAGCCCTCC 146
Qy 43 oPheilleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLe 63
Db 147 CTTAATAGGCACATTACACCTCTCCGCGCCCAAG---CTCCACACACACCTTCCACCAATT 203
Qy 63 uSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValVal 83
Db 204 CTCCCAACGCTACGCGCGCGCTCATCCAGCTCTACTCGCTCGCTCCGCTCGCTGCGC 263
Qy 83 aSerThrProGluLeuPheLysLeuLeuGln*****GluAlaThrSerPhe***Th 103
Db 264 TTCCACGCGCGAATCTCCCGCGAATTCCTCAAGACGACGAA---CTCGACTTCTGTC 320
Qy 103 rArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla*****Pr 123
Db 321 CCGCAAGCACTCCACCGCCCATCGACATCGTCACGTACGACTCTCTCGTTCGCTTCGCGCC 380
Qy 123 o***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu***AsnAlaTh 143
Db 381 GTACGCGCGGCTACTGGAATTCAGAAATTAATGTAATACGAGCTACTGGTGCGCG 440
Qy 143 rThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***Me 163
Db 441 GAACCTGAGCATTTCCAGCCCATTAGAGCTTTGGAGGTCAACAGTTTCTTGAGATTTT 500
Qy 163 tAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeuLysTrp** 183
Db 501 GTACGAGAAACACAGACAGAAACAGAGTGTAAATGTGACTGAGGAGCTTGTGAAGCTGAC 560
Qy 183 *AsnSerThr***SerMetMet***Leu-----GlyGluAl 195
Db 561 GAGTAATGTGATCATCAATGATGTTGGGATCAGGTGTCGGGGACGGAAGGGAGGC 620
Qy 195 aGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuTh 215
Db 621 GGAGGTGCGGAGGACGGTGAAGAGGAGGTGACGACATATTGCGGAGTTGATGTGTC 680
Qy 215 rAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAs 235
Db 681 GGAGATTTGTTGGTTTGTGAAGATTTGGATCTCGAGGGGATTAGAGGAGGTTCGGAGGA 740
Qy 235 pIleLeuAsnLysPheAspProValGluAlaGluValIleLysLysArgArg***IleVa 255
Db 741 TATTAGGAGGAGGTATGATGCTTTGTTGGAGAGATTTATTAGTATGAGGAGGAGGTG-- 798
Qy 255 lArgArgArg***AsnGlyGlu*****GluGlyGlu***serGlyVal***LeuAspTh 275
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Db 799 -AGTTTGAGGGGGGGTGGTGGTGGAGGGTGAAGGAT---TTTTGGATAT 854
Qy 275 rLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile** 295
Db 855 GTTGTGGATGTGATGAGAGTGAAGAAATCGGAGGTGGAGTTTACGAGGAGCATCTCAA 914
Qy 295 *GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTr 315
Db 915 AGCTTTGATCTGGATTTCTTCACTGCGGTACAGACACACAGCAATCAACAGATG 974
Qy 315 pAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Ty 335
Db 975 GGCAATAGCAGAACTCATTAGCAATCCAAATGTACTCAAAAAGCTCAAGAAGAGATGA 1034
Qy 335 rSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIl 355
Db 1035 CAAAGTCATAGGATCAAAAGGTGTTGCAAGAAATCCGACGCCCTTAACCTTGCCTTACCT 1094
Qy 355 eArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLy 375
Db 1095 CAACGGATCATAAAGAAACGTTCCGTCTCCACCTCCCAATCCCATGCTCTACTAGAA 1154
Qy 375 sCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Ph 395
Db 1155 ATCAATTTCTGACGTTGTGTCAACGGGTACACGATCCCTGCCAAAACGCTATTGTTGT 1214
Qy 395 eAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPr 415
Db 1215 CAACCTTTGCTCCATGGAAGAAATCCTAACTACGGAATAATCCGATGAGATTCGACCC 1274
Qy 415 oGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly** 435
Db 1275 CGAGAGTTTCTCGAAGAGG-----ACGGGTCCATAGACGTTAAAGGGCA 1322
Qy 435 *HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAl 455
Db 1323 GCATTTTCGAGTTGCTGCGTTTGGCACGCGGCGGGGTGCGCGGGATGTTGTTAGG 1382
Qy 455 aThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal 475
Db 1383 CATGCGAGGAGTTGTTAGTATTATCGGGGTATGGTGCAGTGTCTCGATTGGAATG-- 1440
Qy 475 uGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAl 495
Db 1441 ----CCGATGCTGTG-----AAGTCGTCGACATGACCGGCGGCC 1478
Qy 495 aGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIle 513
Db 1479 CGGGTTGACGGCTCCACGTGCCAATGATTGTTGTTGTCCTGCAATTTGTCGCCGATT 1533

RESULT 4
US-09-672-785-7
; Sequence 7, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
```

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Perilla frutescens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-09-672-785-7

Alignment Scores:
Pred. No.: 3,54e-117 Length: 1770
Score: 921.50 Matches: 190
Percent Similarity: 57.46% Conservative: 91
Best Local Similarity: 38.85% Mismatches: 183
Query Match: 38.57% Indels: 25
DB: 4 Gaps: 6

US-09-857-581b-66 (1-521) x US-09-672-785-7 (1-1770)

Qy 33 ProAsnProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLys 52
Db 99 CCTACCTCCCGGGCGCTTCCCT---CTTCCATCATCGGCCACTTACACTCTCTCGG 155
Qy 53 AspLysLeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer 72
Db 156 CCGAGA---CTCCACCAACCTTCCAGATCTGTCCCAACGGTACGGGCCCTTAATG 212
Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLys 92
Db 213 CTCCGCTCGGGTCCATCGCTGCTCATCTGCTGCTCGCGGAGCTCGCCAGGAATG 272
Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg 112
Db 273 CTCAAGACACAGAGCTCGTC---TTCCTCCCGCAACACTCCACGCCATGATATC 329
Qy 113 LeuThrTyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheValArg 132
Db 330 GTCACTACGATTATCATCTTCTGCTTCTCCCTACGGGCTTACTGGAAATTCATCA 389
Qy 133 LysLeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArg 152
Db 390 AAATATGACCTACGAGCTGCTCGGGCGCGAAATCTCGCCCACTTTTCAGCCCAT 449
Qy 153 ThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysPro 172
Db 450 ACTCTCGAAGTCAAGCTCTTCTCCAAATCTTATGCGCAAGGGTGAATCGGGGAG 509
Qy 173 LeuAsp***ThrGluLeuLeuLysTrp***AsnSerThr***SerMetMet***Leu 192
Db 510 TTCAACGTGACTGAGAGCTGTGAGCTGACGAGCAACGTCATATCGCATATGATG 569
Qy 193 -----GlyGluAlaGluGluIleArgAspIleAlaArgGlu 204
Db 570 AGCATACGGTGTTCAGACAGCGAGTCGAGCGGAGCGGCGGAGCGGCGGTGATT 629
Qy 205 ValLeuLysIle***GlyLysTrpSerLeuThrAspPheIle***ProLeuLys***Leu 224
Db 630 GTCAACGAGATATTGGGGAGTTCGAGCTCTCCGACATCATATGGCTTTGTAAGA 689
Qy 225 LysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPheAspProValVal 244
Db 690 GATTTCAGGTATAGGAACGGTCCGAGATATCCAGAGAGATATGATGCTCTGCTG 749
Qy 245 GluArgValIleLysLysLysArg***IleValArgArgArg***AsnGlyGlu***** 264
Db 750 GAGAAGATCATCACCGACAGAGAGAAG-----CAGAGCGGACCCAGCGGGGTGC 803
Qy 265 GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspLys 284
Db 804 GCGCGCGGGAAGCAAGGATTTCTTGACATGTTCTTCGACATATGAGAGCGGGA 863
Qy 285 ***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAla 304

864 GCCGAAGTTAAATTCACGAGGAGCATCTCAAAGCTTTGATTTCTGGATTTCTTCC 923
Qy 305 Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro 324
Db 924 GGCACCCACACGACGCGGATCGTGTGTGAATGGCGGATAGCAGAGATGATCAACA 983
Qy 325 ***ValLeu*****AlaArgGluGlu***TySerValValGlyLysAsp***LeuVal 344
Db 984 AATGTGTGAAGAAAGCTCAAGAGAGATTCGCAACATCTCGGATTCGACAGATTC 1043
Qy 345 AspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArg 364
Db 1044 CAAGAATCCGACGCCCAATCTGCCCTACCTTCAAGCCCTCATCAAGAAACATTC 1103
Qy 365 MetHisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly 384
Db 1104 CTCACCTCCCAATCCCAATGCTGGCGAGGAATTCGATCTCCGACTCGCTCATCG 1163
Qy 385 ***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp 404
Db 1164 TACATGATTCCGCAACACGCTCTCTTCTGTCACCTCTGTCCTCGGCGGAGAC 1223
Qy 405 LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGlu 424
Db 1224 AAAATCTGGGACTACCCGACGCGGCTTCCAGCGGAGAGGTTTCTGGAGAAG----- 1274
Qy 425 GlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySer 444
Db 1275 ---GAAAGGCGGCATCGATGTTAAAGGGCAGCATTTTGAGCTGTACCGTTCC 1331
Qy 445 GlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAla 464
Db 1332 GGCAGGAGAGCTGCCAGGAGTGCTTTAGCCATTCAGAGGTGTCATCATTAATGG 1391
Qy 465 SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484
Db 1392 ACGATGATTCAATGCTTCGATTCGAAGCTG-----CCGACGCG----- 1430
Qy 485 ***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer 504
Db 1431 ---TCCGCGCATGTTGATATGGCAGAACGCGGCTCAGGCAACCGCGAGACCG 1487
Qy 505 LeuValCysValProLeuAlaArgIle 513
Db 1488 TTGTTTCCGCTGCTGCGCGCGGTT 1514

RESULT 5
US-09-142-108C-16
; Sequence 16, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
; APPLICANT: Brugnolera, Filippa
; APPLICANT: Holton, Timothy A.
; APPLICANT: Michael, Michael Z.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 11658
; CURRENT APPLICATION NUMBER: US/09/142.108C
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: P8386
; PRIOR FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Chrysanthemum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(1530)
US-09-142-108C-16
```

Alignment Scores:

Pred. No.: 8,12e-78 Length: 1660
 Score: 637.50 Matches: 162
 Percent Similarity: 49.81% Conservative: 101
 Best Local Similarity: 30.68% Mismatches: 208
 Query Match: 26.68% Indels: 57
 DB: 4 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-142-108C-16 (1-1660)

QY 5 LeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro***Ala 24
 Db. 34 CTCATCTCGGG---TCAGTACTATGTTTCTTAACCTA-----72
 QY 25 ***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro-----Arg 41
 Db 73 AGTTTCAGTAATCCGCGACGACTCCACCGCGGCAACACCATGGCCCTATAGTCGGGAAC 132
 QY 42 LeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***Ile 61
 Db 133 TTACCACACCTTGGC-----CCATCCACACGACGACTCGCG 171
 QY 62 AspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrVal 81
 Db 172 GCCTTAGCCAAAGAGTACCGGCGCCATTCATGCACCTCGCGCTCGGTGTGGACGTGGTT 231
 QY 82 ValAlaSerThrProGluLeuPheLeuPheLeuGln*****GluAlaThrSerPhe 101
 Db 232 GTGCGCGCGTGTGTCCTCGTAGTGCACAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTT 288
 QY 102 ***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
 Db 289 GCTAGTAGCGCGCAAAATCTGCGCGCAACATGTGCGGTATATATACAGTCTGTG 348
 QY 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuLeuMetAsnAspLeu*** 140
 Db 349 TTTGCACCTTATGCTCCAGGTGCGGTGTTTAAAGGAAGATTGTTTCCGTCCATTTGTTT 408
 QY 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
 Db 409 TCGCTTAAGCACTTGATGATTTTCGTCATGTCGACGAGGAGGTAGCGAGTCTTAACC 468
 QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
 Db 469 CGGTACTACTAGTGTGGAACCTCA-----CGGTACAGCTTGGCCAACTACTTAAC 522
 QY 181 LysTrp***AsnSerThr***SerMetMet***LeuGly-----193
 Db 523 GTGTGTGCCCAAAACGCTTAGCACGCGGTAAATGTAGTAGAGAGAGTTCGCGAGACGGA 582
 QY 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***Gly 210
 Db 583 ATTGACAGGTGACCGCAATAGTTCAAAGATAGTGTAGTAGAGTAATGTATGATTAGCAGGA 642
 QY 211 GluTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGlu 230
 Db 643 GAATTAACCTTGGTGACTTATTCCTGTACTTGCACCTATTCACCTACAGGCATTA 702
 QY 231 LysArgIleAspIleLeuAsnLysPheAspProValGluArgValIleLysLys 250
 Db 703 AAAAAAATGAAGAGCTTCATGTTCCGTTCCGTTCCATTTCTTAGTAAGATCGTTGAGGAG 762
 QY 251 ArgArg***IleValArgArg***AsnGlyGlu*****GluGlyGlu***SerGly 270
 Db 763 CATAAAG-----GCACCTGGTGGTGGTGGTGCATACT 795
 QY 271 Val***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***Glu---IleLysIle 289
 Db 796 GATTTGCTGACGAGCTTGATTTTACCTTAAGATGATGCTCATATTGAGTGGGAGCTT 855
 QY 290 ThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSerThr 309
 Db 856 ACAGATACTGAATCAAGCTTTGCTTCTGAATTTATTCGTCGCGGAACACAGACATCC 915

QY 310 Ala*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu***** 329
 Db 916 TCTAGTACAGTAGAATGGGCAATAGCGCAACTCATTCGTCTCAACAATATTAAACAA 975
 QY 330 AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThr 349
 Db 976 GCCGAGAGAGATAGACGCTGTAGTTGGTCAAGACCGGCTTTAACAAGATTGGACTTG 1035
 QY 350 GlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeu 369
 Db 1036 AGCCAACATACATACCTCCAGGCTCTTGTGAAGAGAGGTGTAGGCTCCACCTTCAACG 1095
 QY 370 ProVal---ValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro 388
 Db 1096 CCATCTCTCTTACCAAGATATCATCCGAGAGTGTGAGGTGAGTATATATATCCCT 1155
 QY 389 GluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAsp 408
 Db 1156 AAGGATCCACACTCTCTCGTTAAGCTGTGGCCATTGCGCGAGACCCAAAAATGTGGCG 1215
 QY 409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428
 Db 1216 GATCCTCTTGAATTTAGGCTTCTCGGTTTTTA-----CCCGGGGAGAAAGCC 1266
 QY 429 ***LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448
 Db 1267 GTGCTGATGTAGGGGAAATGATTTGAAGTTATACCATTTGGGCGAGCAAGGATT 1326
 QY 449 CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468
 Db 1327 TGTGCGGTATGACCTAGCTAGCTTGAGATGCTCAGTGTCTCATTCACATTTGGTCAA 1386
 QY 469 CysPheAspLeuGlnVal-----LeuGlyProGlnGlyGlnIleLeuLysGly*** 485
 Db 1387 ACTTTTGAATTTGGAACTGCTACCGGTTAGACCGGAG-----1425
 QY 486 AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeu 505
 Db 1426 -----ATGCTCAACATGAAGAAGCGTATGGATTGACCTTCAACGGGCTGCACCTTG 1479

RESULT 6

US-09-689-783A-1
 ; Sequence 1, Application US/09689783A
 ; Patent No. 6605469
 ; GENERAL INFORMATION:
 ; APPLICANT: KANG, JEONG-GU
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A CYTOCHROME P450 HYDROXYLASE IN
 ; FILE REFERENCE: 107572
 ; CURRENT APPLICATION NUMBER: US/09/689,783A
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1488
 ; TYPE: DNA
 ; ORGANISM: Pisum sativum
 US-09-689-783A-1

Alignment Scores:
 Pred. No.: 1.03e-76 Length: 1488
 Score: 629.00 Matches: 154
 Percent Similarity: 49.79% Conservative: 87
 Best Local Similarity: 31.82% Mismatches: 199
 Query Match: 26.33% Indels: 44
 DB: 4 Gaps: 12


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Qy 41 -----ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHis 57
Db 244 ATCTCGGAATCTGCCACATCTTGGCCGAGGCC-----CAC 282
Qy 58 TyrAla***IleAspLeuSerLysLysGlyHisGlyProLeuPheSer*****PheGlySer 77
Db 283 CAGTCGATGGCGCGCTGGCAGCGGTGCAGCGCCATTAATCTCAAGATGGCGTTT 342
Qy 78 MetProThrValValAlaSerThrProGluLeuPheLysLeuLeuGln*****Glu 97
Db 343 GTGCATGTGGTGTGGCTCTCTCAGCATCGCTGGGAGAAATTTCTGAAGGTGCATGAC 402
Qy 98 AlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyArgPhe--- 116
Db 403 GCA---AACTCTCGAGCAGCGCTCCCAATTCGGTGCAGAAACACAGTGGCTCAACTAT 459
Qy 117 *****ValAla*****Pro***GlyProTyTrp***PheValArgLysLeuLeuMet 136
Db 460 CAGGACTTGGTCTTGTCTCTTATGGCCCGCTGGCGGATGCTCAGGAAATCTGTGCA 519
Qy 137 AsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIle 156
Db 520 CTCACCTCTCTCCGCCAAGCCTTGAACGACTTCACACAGTCACAGAGATGAGGTG 579
Qy 157 ArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***Thr 176
Db 580 GGGATCTCTACTCGCTTCTAGCAGATCGAGGAAACG-----CGTTGAATATAGGG 633
Qy 177 GluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly----- 193
Db 634 CAGATGATGAACATCGCCCAACCAATGCAATAGCGGTGTATGTGGTTCGACGGGTG 693
Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLys 207
Db 694 GTTGGCAGCAGACTCAAGCGCGGAGGAGTTTAAGCAATGTGTAGTGGATGGTA 753
Qy 208 Ile***GlyGluTyTrpSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
Db 754 TTAGCTGGTGTGTCAACTAGGTGATTTATCCCACTCTTGAAAAATTTGGATCTCAA 813
Qy 225 -----LysValGlyLysTyTrpGluLysArgIleAspAspIleLeuAsnLysPhe 240
Db 814 GGTGTCTATGCTAAGATGAAGAAGCTTCACTTGGTTTCGACTCGTCTTGGATGAG--- 870
Qy 241 AspProValValGluArgValIleLysLysArg***IleValArgArgArg***Asn 260
Db 871 -----ATCCTTGGAGACCAAGATC 891
Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
Db 892 AACAGCTCAGATGAACCAAGGCCATTCGGATTTGTGAACATGTTAATTTCTTTGAAG 951
Qy 281 Glu---AspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValVal 299
Db 952 GAGCTGATGATGCGGAAGGAGGAGGCTCAGCGAGTACCGAGCTAGAAATTTAAAGCGTCTG 1011
Qy 300 Asp***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGlu 319
Db 1012 AACTGTTTCTGTCAGAGACTGACACAACTCAAGCACTGTGGAATGTGCAATGCTGAG 1071
Qy 320 LeuIleAsnAsnPro***ValLeu*****AlaArgGluLys***TyTrpValValGly 339
Db 1072 TTAGTACGACATCTGGAATCTTGCCTCAAGTCCAAAGAACTCGACTCTGTGTGGT 1131
Qy 340 LysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyTrpIleArgAlaIleVal 359
Db 1132 AAGAAATCGGTGTGGAAGGAGGTGATCTGCGCGGATTAACCAATCTCTCAAGCGGTGTC 1191
Qy 360 LysGluThrPheArgMetHisProProLeuProVal---ValLysArgLysCys***Glu 378
Db 1192 AAGAAATTTCCGACTCCATCTCCACCCCGCTCTCCCTACCGAGATCGCACATGAG 1251
Qy 379 GluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrp 398
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Db 1252 AGTTGTGAAGTGAATGATGACTTGAATTCGAAGGGTTCGACACTTCTTGTCAATGTTGG 1311
Qy 399 GlnValGly***Asp***LysTyTrpAspArgProSerGlu***ArgProGluArgPhe 418
Db 1312 GCAATGTCTCGCATCAAAATGTGTGGATGAACCACTAGAGTTCCGCGCTGAACGATTC 1371
Qy 419 LeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGln 438
Db 1372 TTGAAG-----GGCGGGGAAAGCCCTAAATGTGATGTTAGAGGAAATGATTTCCGA 1422
Qy 439 LeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly 458
Db 1423 TTGATACCGTTCGGAGCGGCCGAGAAATTTGTGCAGGAATGAGCTTAGGAATACGTATG 1482
Qy 459 ***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGln 478
Db 1483 GTCAGTGTGTGACAGCAACTTTGAACCATGCGCTTTGACTTTGATTTG-----GCGGAT 1536
Qy 479 GlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThr 498
Db 1537 GGACAGTTG-----CTGAAAGCTTAAACATGGAGGAAGCTTATGGGCTGACC 1584
Qy 499 ValProArgAlaHisSerLeuValCysValProLeuAlaArg 512
Db 1585 TTGCAACGAGTCAACCTTTGGTAGTGCACCCGCAAGCCTAGG 1626

RESULT 8
US-09-499-302A-1
; Sequence 1, Application US/09499302A
; Patent No. 6369212
; GENERAL INFORMATION:
; APPLICANT: BOUNG-JUN, OH
; APPLICANT: MOON, KYUNG KO
; APPLICANT: YOUNG, SOON KIM
; TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
; TITLE OF INVENTION: INCOMPATIBLE INTERACTION
; FILE REFERENCE: 10324/P64443USO
; CURRENT APPLICATION NUMBER: US/09/499,302A
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-499-302A-1

Alignment Scores:
Pred. No.: 4.92e-76 Length: 1781
Score: 625.00 Matches: 151
Percent Similarity: 49.28% Conservative: 89
Best Local Similarity: 31.01% Mismatches: 211
Query Match: 26.16% Indels: 36
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-499-302A-1 (1-1781)
Qy 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeu-----Lys 52
Db 100 CTTCTCTGGTCCATGG---AAATTTACCTTTTATTTGAAGCCTACATCATCTTGGCGCTGAC 156
Qy 53 AspLysLeuLeuHisTyAla***IleAspLeuSerLysLysHisGlyProLeuPheSer 72
Db 157 GTTCCACTTCTCTCATCATCATCGCTTAAATAATCTAGCAAACTTTATGGCGCTGATGCAC 216
Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe 92
Db 217 TTACGACTCGGGAAATTTCTACCGTCACTATTTCTCCCGCGAATGGCAAGGAAGTA 276
Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
Db 277 CTAAAAAATCAGCAGC---CTCGCTTTTCGCAACGAGGCCGAAACTTGTGTGGTGTGATC 333
```


Qy 113 LeuThrTyrAsp*****Valala*****Pro***GlyProTyrTrp***PheVal 131
Db 334 GTCCATTATGATAGTACGATAGTATGCTTCTCCATATGCTGAATAGTACGAGCAGATT 393
Qy 132 ArgLysLeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeu 151
Db 394 CGTAAATTTTCATCTGCAATCGAACTCTTAGTCCCAAGATGGTCAAAATTTCTTAGCTCAAT 453
Qy 152 ArgThrGlnGlnIleArg-----Lys***LeuArg***MetAlaGln***AlaGlu 168
Db 454 CGCAGGATGAGTGTGATGATGCTCATCTATACGAACCATGCCAAATTT----- 507
Qy 169 Ala***LysProLeuAsp***ThrGluGluLeuLysTrp***AsnSerThr***Ser 188
Db 508 -----CCGCTCAACCTTACAGACAAATATTTGTTTACAAAGTTCGTAATCTGT 558
Qy 189 MetMet***LeuGly-----GluAlaGluGluIleArgAspIleAlaArgGlu 204
Db 559 AGATCAGCTCTGGGAAATAATATGCTGACCAAGACAACTGATAATTTTTCATGAGGAA 618
Qy 205 ValLeuLysIle***GlyLysTrpSerLeuThrAspPheIle***ProLeuLys***Leu 224
Db 619 ATAATATCAITGACAGGTGGATTTAGTATTTCTGATTTTTCCTACATGGAATAATGCTA 678
Qy 225 ---LysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPheAspProVal 243
Db 679 CATGATGTTGGTGTCAAAACTAGACTGCTGAAGCTCATCTGTAATAATCGATGATT 738
Qy 244 ValGluArgValIleLysLysArgArg***IleValArgArg***AsnGlyGlu*** 263
Db 739 TTGGAACATGTAGTGAATGACACAAA-----CAGAATCGAGCGATGGCCAAAG 789
Qy 264 ***GluGlyGlu***SerGlyVal***Leu---AspThrLeuLeuGluPheAlaGluasp 282
Db 790 GGTAAATGCGAATTTGGCGGTGAAGATTGTATGATGTTTGTCTAAGGGTTTCGAGAAGT 849
Qy 283 GluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***Phe 302
Db 850 GGAGAGTTCAATTTCCATCAGGATGACATATCAATCAATCAATATGATGACATGTTTC 909
Qy 303 SerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsn 322
Db 910 TCCGCTGATCTGAAACGCTCATCGCAACTATAATTTGGCATTAGCTGAAATGATGAAG 969
Qy 323 AsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysasp*** 342
Db 970 AAACCAAGTGTCTAGCAAGGCAACAGCTGAAGTGAGACAAAGTCTTGAAGGAAAGAAA 1029
Qy 343 LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThr 362
Db 1030 GGTITTCACAAATGATCTGTGATGAGTGTGAAGTACTTGAAGTGTGATTAATCAAGAACT 1089
Qy 363 PheArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys*** 381
Db 1090 CTAAGATGACCCCTCCCAATTTCTTATTAGTCCCTAGAGAATGTATCAAGGATACAAAG 1149
Qy 382 IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValgly 401
Db 1150 ATTGACGGGTACAATATACCTTTCAAAACTCGAGTCATAGTTAATGCAATGGGCAATGGA 1209
Qy 402 ***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr 421
Db 1210 CGAGATCTCTGAAGTGTGGATGACCTGAAAGCTTTTCCCGAGAGATTC----- 1260
Qy 422 ***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuPro 441
Db 1261 -----GAGAAATGTTCTGTGATCTTCTTGGAGCCATCATCAATTTATTCCA 1308
Qy 442 PheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThr 461
Db 1309 TTGTGTGGGGAAGAAGGATTTGCTCTGGAATGCTTTTGTGTTTAGCCAATTTGGACAA 1368

Qy 462 LeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIle 481
Db 1369 CCATTAGCTCAATTTACTTTATCTTCACTTCGATCGGAACCTC-----CCTAATGGACAAAGT 1422
Qy 482 LeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArg 501
Db 1423 CACGAAATTTGGAC-----ATGACGAGGTCACTCGAATTTCTGCACACAAGA 1470
Qy 502 AlaHisSerLeuValCysVal 508
Db 1471 AAGGATGATCTGTTTGTGATT 1491
RESULT 9
US-09-142-108C-14
; Sequence 14, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
; APPLICANT: Brugniera, Filippo
; APPLICANT: Holton, Timothy A.
; APPLICANT: Michael, Michael Z.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 11658
; CURRENT APPLICATION NUMBER: US/09/142,108C
; CURRENT FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: P8386
; PRIOR FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1748
; TYPE: DNA
; ORGANISM: Rosa hybrida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(1563)
US-09-142-108C-14
Alignment Scores:
Pred No.: 9,04e-76 Length: 1748
Score: 623.00 Matches: 161
Percent Similarity: 48.73% Conservative: 89
Best Local Similarity: 31.38% Mismatches: 205
Query Match: 26.08% Indels: 58
Gaps: 16
US-09-857-581B-66 (1-521) x US-09-142-108C-14 (1-1748)
Qy 27 LysAlaLeuArgHis---LeuProAsnProProSerPro***ProArgLeuProPheIle 45
Db 88 AAATCCCAAGCCACTCGCTCCCTCTCCTCGCCCAACCA---TGGCCGGTGGTT 144
Qy 46 GlyHis*****HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSer 64
Db 145 GGCAACTTACCTCACTTG-----GGCCCTTCGCCACCACTCATCGCGAGTTGGCG 198
Qy 65 LysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSer 84
Db 199 AAGAAACACGGCCGCTCATGCACCTCGGCTCGGTACGTGAGTGTGAGTGTGCGGCA 258
Qy 85 ThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArg 104
Db 259 TCAGCATCCGTCGGCGCCAGTCTTCTGAAGACTCAGACGCC---AATTTCTCCAGCCGA 315
Qy 105 PheGlnThrSerAla***Arg***LeuThrTyrAsp-----Valala*****Pro 123
Db 316 CCGCCCAACTCCGGCGCCAGCACCTCGCTTATACTACAGGACCTCGTGTTCAGGCCG 375
Qy 124 ***GlyProTyrTrp***PheValArgLysLeuIleMetAsnArgLeu***AsnAlaThr 143
Db 376 TACGCTCCACGGTGGCGCATGTTCCGGAAGATGACCTCCGTCATCTCTTCTCCGGCAA 435
Qy 144 ThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***Met 163

Qy 26 SerLysAlaLeuArgHisLeuProAsnProProSerPro***ProArgLeuProPheile 45
Dy 101 TCGAATATCCCAACAAACCTA-----CCTCCGAGCCCT---CCGAAGCTCCCGTGATC 151
Qy 46 GlyHis***HisLeuLeuYsAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65
Dy 152 GCCACCTCCCACTTCCTCTGGGGAGGCTTCCCGACACAGTGTATTAGAGCATAGCCAG 211
Qy 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
Dy 212 AAGTACGGCGCGGTGGCCACGTCGAGCTGGAGAGTGATCTCGTGGTCTCTCGTCG 271
Qy 86 ProGluLeuPheLeuLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
Dy 272 GCGGAGGCGAGCAAGCAGCGCATGAAGGTGCTGGAC---CCGAACCTTCGCCGACCGGTTC 328
Qy 106 GlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla*****Pro*** 124
Dy 329 GACGGCATCGGGTCCAGGACCATGTGGTACCAAGATGATCATCTTCAGGCCCTTAC 388
Qy 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThrThr 144
Dy 389 AACGATCACTGGCCGAGATCGGAGGATCTGCGTACAGAGCTGCTGAGCCCGAAGAC 448
Qy 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
Dy 449 GTCAGGCTCTTCGGGTACATAAGCAGGAGGATCGAGCGCTCATCGGCTCTCGGG 508
Qy 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp***Asn 184
Dy 509 TCGTCGGGGGAGCG-----CCGGTCAGCTGACGAGGAGGTGTGCAAGATCTCGTGT 562
Qy 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
Dy 563 GTCGTGTGTCCAGGCGCGGCTTCGGAGGTGTCTCAAGGACCGAGGTTCGTTGGCGGAG 622
Qy 201 IleAlaArgGluValLeuLysile***GlyLysTrpSerLeuThrAspPheile***Pro 220
Dy 623 TTGTGAAGGAGTCTGTCGATCGGCTCGCGGTTCGAGCTGCGGAT---CTCTACCT 679
Qy 221 -----LeuLys***LeuLysValGlyLysTyrGluLysArgLysAspLys 236
Dy 680 TCCTCATGGCTCTCAACCTGCTAGCTGTAACAAGTAC-----AGGTTGACAGGATG 733
Qy 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArg***IleValArg 256
Dy 734 CGCGCGCGCTCATCATCTTGTGTTGGTCTCGAGGAGCATAGG-----781
Qy 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
Dy 782 -----GAGAAGAAGAGCGCGGAGTTCGAGGCGAGGACATCGTCGACGTT 826
Qy 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile*** 295
Dy 827 CTTTTCAGGATGCAAGAGCGGCGACATCAAAATTCCTATTCTTCAATTGATCAAG 886
Qy 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
Dy 887 GGTTCATTTCGACACCTTCTCGCGGAGCTGAACGCTCTTCAGCAGCATCTCATGG 946
Qy 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
Dy 947 GCGTGTTCGGAATGATGAGGATCCGCGAAGATGGCAAGTTCGAGCGGAGGTGAAGA 1006
Qy 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle 355
Dy 1007 GAGCGCTCAGGGAAGACAGACTCGTGTGATTTGACGCGAGGTGCAAGACTAAATACCTG 1066
Qy 356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
Dy 1067 AGATCGGTGTTAAGGAGACTCTGAGGCTGCACCCCTCCCTTTTCATTAAATCCCAAGACAA 1126

Qy 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
Dy 1127 TCAGGGAAGAATCGGAGGTAAACGGGTACACGATTCCGGCCAAACTAGAAATCTTTCATC 1186
Qy 396 AsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPro 415
Dy 1187 AACGCTCTGGGCTATCGGAAGGATCCCAATACCTGGGAAGATCTGCGGCTTACATTCGGCCT 1246
Qy 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
Dy 1247 GAGAGATTCGATGAGTTTCCAGG-----GATTTTCATGGGAAC 1285
Qy 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
Dy 1286 GATTTCGAGTTTCATCCCATTCGGGCGGTCGAAGAATCTGCCCGGTTTACATTCGGG 1345
Qy 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
Dy 1346 CTGGCAATGTTGAGATCCCATTCGGCAACTGCTCTACCACTTCGACTGGAAATG--- 1402
Qy 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
Dy 1403 ---CCACAAGGAATG-----ACTGATCCGACTTGGACATGACGAGACCCCA 1447
Qy 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
Dy 1448 GGTCTTCTCGGCCAAAAAGAAAAATGTTTGTCTTGGTTGCC 1489

RESULT 11

US-09-292-768-1
; Sequence 1, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE OF INVENTION: LIMONENE HYDROXYLASES
; FILE REFERENCE: wbur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Mentha spicata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1507)
US-09-292-768-1

Alignment Scores:
Pred. No.: 3,86e-75 Length: 1762
Score: 618.50 Matches: 146
Percent Similarity: 48.38% Conservative: 93
Best Local Similarity: 29.55% Mismatches: 214
Query Match: 25.89% Indels: 41
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-292-768-1 (1-1762)

Qy 26 SerLysAlaLeuArgHisLeuProAsnProProSerPro***ProArgLeuProPheile 45
Dy 101 TCGAATATCCCAACAAACCTA-----CCTCCGAGCCCT---CCGAAGCTCCCGTGATC 151
Qy 46 GlyHis***HisLeuLeuYsAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65
Dy 152 GCCACCTCCCACTTCCTCTGGGGAGGCTTCCCGACACAGTGTATTAGAGCATAGCCAG 211
Qy 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
Dy 212 AAGTACGGCGCGGTGGCCACGTCGAGCTGGAGAGTGATCTCGTGGTCTCTCGTCG 271
Qy 86 ProGluLeuPheLeuLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
Dy 272 GCGGAGGCGAGCAAGCAGCGCATGAAGGTGCTGGAC---CCGAACCTTCGCCGACCGGTTC 328
Qy 106 GlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla*****Pro*** 124
Dy 329 GACGGCATCGGGTCCAGGACCATGTGGTACCAAGATGATCATCTTCAGGCCCTTAC 388
Qy 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThrThr 144
Dy 389 AACGATCACTGGCCGAGATCGGAGGATCTGCGTACAGAGCTGCTGAGCCCGAAGAC 448
Qy 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
Dy 449 GTCAGGCTCTTCGGGTACATAAGCAGGAGGATCGAGCGCTCATCGGCTCTCGGG 508
Qy 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp***Asn 184
Dy 509 TCGTCGGGGGAGCG-----CCGGTCAGCTGACGAGGAGGTGTGCAAGATCTCGTGT 562
Qy 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
Dy 563 GTCGTGTGTCCAGGCGCGGCTTCGGAGGTGTCTCAAGGACCGAGGTTCGTTGGCGGAG 622
Qy 201 IleAlaArgGluValLeuLysile***GlyLysTrpSerLeuThrAspPheile***Pro 220
Dy 623 TTGTGAAGGAGTCTGTCGATCGGCTCGCGGTTCGAGCTGCGGAT---CTCTACCT 679
Qy 221 -----LeuLys***LeuLysValGlyLysTyrGluLysArgLysAspLys 236
Dy 680 TCCTCATGGCTCTCAACCTGCTAGCTGTAACAAGTAC-----AGGTTGACAGGATG 733
Qy 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArg***IleValArg 256
Dy 734 CGCGCGCGCTCATCATCTTGTGTTGGTCTCGAGGAGCATAGG-----781
Qy 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
Dy 782 -----GAGAAGAAGAGCGCGGAGTTCGAGGCGAGGACATCGTCGACGTT 826
Qy 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile*** 295
Dy 827 CTTTTCAGGATGCAAGAGCGGCGACATCAAAATTCCTATTCTTCAATTGATCAAG 886
Qy 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
Dy 887 GGTTCATTTCGACACCTTCTCGCGGAGCTGAACGCTCTTCAGCAGCATCTCATGG 946
Qy 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
Dy 947 GCGTGTTCGGAATGATGAGGATCCGCGAAGATGGCAAGTTCGAGCGGAGGTGAAGA 1006
Qy 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle 355
Dy 1007 GAGCGCTCAGGGAAGACAGACTCGTGTGATTTGACGCGAGGTGCAAGACTAAATACCTG 1066
Qy 356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
Dy 1067 AGATCGGTGTTAAGGAGACTCTGAGGCTGCACCCCTCCCTTTTCATTAAATCCCAAGACAA 1126


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Db 212 AAGTACGGGGCGGTGGCGCAGCTGCTGACCTGGGAGAACTGACTCGGTGGTGGTCTGCTGCTG 271
Qy 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
Db 272 GCGGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 328
Qy 106 GlnThrSerAla***Arg***LeuThrTyArgPhe*****ValAla*****Pro*** 124
Db 329 GACGGCATCGGGTCCAGGACCATGTGTGTACGACAAAGATGAGATCATCTTCAGCCCTTAC 388
Qy 125 GlyProTyArgPhe***PheValArgLysLeuLeuMetAsnAspLeu***AsnAlaThrThr 144
Db 389 AACGATCAGTGGCGCCAGATGCGGAGGATCTGCTGACAGAGCTGTGAGCCCGGAGAAC 448
Qy 145 ValAsn***LeuArgProLeuArgThrGlnGlnLeuArgLys***LeuArg***MetAla 164
Db 449 GTCAGGTCTTCGGGTACATAAGGAGGAGGAGATCGAGCGCCTCATCCGGCTGCTCGGG 508
Qy 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeuLysTrp***Asn 184
Db 509 TCGTCCGGGGGAGCG-----CGGTGACGTGACGCGAGGAGGTGTGCAAGATGTCGTGT 562
Qy 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluLeuArgAsp 200
Db 563 GTCTCTGTGCGAGGGCGGCGGTTCGGGAGGTGCTCAAGGACGAGGTTGCTGTGGCGGAG 622
Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTySerLeuThrAspPheIle***Pro 220
Db 623 TTGGTGAAGAGTCTGTGGCATTTGGCTCGGGTTGAGCTGGCGGAT---CTCTACCT 679
Qy 221 -----LeuLys***LeuLysValGlyLysTyArgLysArgLysAspIle 236
Db 680 TCCTCATGGTCTCTCAACCTGCTTAGCTTGAACAAGTAC-----AGGTTGCGAGGATG 733
Qy 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
Db 734 CGCGCGCGCTCGCATCATCTCTGATGGTTCCTGGAGGAGCATAGG-----781
Qy 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
Db 782 -----GAGAGAGAGAGCGGCGAGTTTGGAGCGGAGGAGCATCTGTCGAGTT 826
Qy 276 LeuLeuGluPheAlaGluAspGluThr***GluLeuLysIleThrLys*****Ile*** 295
Db 827 CTTTTCAGGATGCAAGAGGCGAGGACATCAAAATTCCTTACTTCCATTTGATCAAG 886
Qy 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
Db 887 GGTTCATTTTCGACACCTTCTCGCGGAGGAGTGAACGCTTTCGACGACCATCTCATGG 946
Qy 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
Db 947 GCGTTGTCGAGACTGATGAGATCCGCGGAGAGATGCCAAGGTGCGAGCGGAGGTAGA 1006
Qy 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyIle 355
Db 1007 GAGCGCTCAAGGAAAGACAGTCTGATTTGAGCGAGGTGCAAGAGCTAAATAACTCTG 1066
Qy 356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
Db 1067 AGATCGGTGTAAAGGAGACTCTGAGGCTGCACCTCCCTTTCATTAATCCCAAGACAA 1126
Qy 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
Db 1127 TCAGGGAAGATGCGAGGTTAACGGGTACAGATTCCGGCCAAACTAGAACTTTCATC 1186
Qy 396 AsnValTrpGlnValGly*****Asp***LysTyTrpAspArgProSerGlu***ArgPro 415
Db 1187 AACGTCTGGGTATCGGAGGAGTCCCACTACTGGGAGATCCCGACACCTTCGCGCCT 1246
Qy 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
Db 1247 GAGAGATTCGATGAGGTTTCCAGG-----GATTTCATGGGAAAC 1285
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Qy 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
Db 1286 GATTCGAGTTTCATCCATTCGGGGCGGTGCGAAGAATCTGCCCGGTTTACATTCGGG 1345
Qy 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
Db 1346 CTGCGAAATGTTGAGATCCCATTTGGCGCAACTCTCTTACCACCTCGACTCGAAATG--- 1402
Qy 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
Db 1403 ---CCACAGGAATG-----ACTGATGCCACTTGGACATGACGGAGACCCCA 1447
Qy 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
Db 1448 GGTCTTTCTGGGCCAAAGAAAAAATGTTTGCTTGCTTCCC 1489
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RESULT 13

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US-09-351-229-3
; Sequence 3, Application US/09351229
; Patent No. 6380465
; GENERAL INFORMATION:
; APPLICANT: Barrett, Michael
; TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and
; FILE REFERENCE: P-1049
; CURRENT APPLICATION NUMBER: US/09/351,229
; EARLIER FILING DATE: 1999-07-11
; EARLIER APPLICATION NUMBER: 60/092,596
; EARLIER FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Zea mays
US-09-351-229-3
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Alignment Scores:

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Pred. No.: 4-7e-75 Length: 1806
Score: 618.00 Matches: 164
Percent Similarity: 50.40% Conservative: 90
Best Local Similarity: 32.54% Mismatches: 199
Query Match: 25.87% Indels: 52
DB: 13 Gaps: 13
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US-09-857-581B-66 (1-521) x US-09-351-229-3 (1-1806)

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Qy 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
Db 86 CCGCGGGCGCCCAAGCCA---TGGCGGATCATCGCAACCTTAACCTCATG---GGCGAG 139
Qy 55 LeuLeuHisTyAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db 140 CTCCCCACCGCTCCCAAGAACGAGCTCTCCAAAGCGGTACGGTCCGCTCATGCGACTCTGG 199
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheGln 94
Db 200 TTCGGGTGCTGCTGCTGTGCTGCGCGCGCTCCCGGAGATGCCAAGAGCTTCTCTCAAG 259
Qy 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 260 ACCAAGCAGCGC---GCGTTCTCCGACCGCGCGAGGTTCGACGTCCGCAAGTACACCGCG 316
Qy 115 TyrAsp---*****ValAla*****Pro***GlyProTyTrp***PheValArgLys 133
Db 317 TACGACTGCTCCGCGCTTCTGTGGGTCTCTTTTGAAGCGCTACCTGCGCCAGGACGCGAG 376
Qy 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 377 ATCTGGCGCCACCGAGCTCTTCAGGCCACCGCGGCTCGAGTCTCTCGAGCATCCCGGAC 436
Qy 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
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Db 241 CTCGGCAGGTTCTCCGTCGTCTCCGTCGCCGAGGCCAGAGGAGCGCATGAAG 300
Qy 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 301 CTGCTGGAC---CCGGCTCGCGGACCGGTTTCGAGAGCATCGGAGCAGAGATCATGTGG 357
Qy 115 TyrAsp-----ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
Db 358 TACGACAAACGACGACATCATCTTCAGGCCCTTACAGCGTGCACATCGCGCCAGATCGGAAG 417
Qy 134 LeuileMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 418 ATCTGCGTCTCCGAGCTCCTCAGCGCCGCAACCTCCGCTCTTCCTCGGCTTCATCAGCGAG 477
Qy 154 GlnGlnileArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 478 GACGAGGTGTCGCCCTCCTCGGCCACCTCGCTCCGTCCTCGCGCGGGGGGCGCGTG 537
Qy 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
Db 538 GACCTCAGGAGCGGATGACGACGCTGACGTGCTCCATCTGTCAGCGCGCGGCTTCGGG 597
Qy 194 -----GluAlaGluLysLeuLeuLysTrp***ProLeuLys***Leu----- 224
Db 598 AGCGTGATCAGGACCGACGAGAGCTGTGTGAGAGCGGAGCGCCCTCAGCATGGCG 657
Qy 210 GlyLysThrSerLeuThrAspPheile***ProLeuLys***Leu----- 224
Db 658 TCCGGGTTCGAGCTCGCGGACATGTTCCCTCCTCCAGCTCCTCACTGCTCTGCTGG 717
Qy 225 -----LysValGlyLysTyrGluLysArgileAspAspLysLeuAsnLysPheAsp 241
Db 718 AACAAAGCAAGCTGTGGAGGATCGCGCGCTGACGCGCATCTCTCGAGGCCATC--- 774
Qy 242 ProValValGluArgValLysLysLysArgArg***IleValArgArgArg***AsnGly 261
Db 775 ---GTGAGGAGCAACAGCTCAAGAG----- 798
Qy 262 Glu*****GluGlyGlu***SerGlyVal---***LeuAspThrLeuGluPheAla 280
Db 799 -----AGCGCGAGTTGGCGGAGGACATTAATGACGTACTCTTAGGATCGAG 849
Qy 281 GluAspGluThr***GluileLysileThrLys*****Ile***GlyLeuValValAsp 300
Db 850 AAGGATAGCCAGATCAAAAGTCCCATCACCACCAACGCCATCAAGCCTTCATCTTCGAC 909
Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
Db 910 ACGTTCTCAGCGGGGACCGGACATCATCAACCAACCCCTGTGGTGATGGCGGAGCTG 969
Qy 321 IleAsnAsnPro***ValLeu***AlaArgGluGlu***TyrSerValValGlyLys 340
Db 970 ATGAGGAATCAGAGGTGATGGCGAAGAGCGGAGGTGAGAGCGCGCTGAAAGGGG 1029
Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1030 AAGACCGACTCGGACGTGGACGACGTGCAGGAGCTTAAGTACATGAATCGGTGCTGAAG 1089
Qy 361 GluThrPheArgMetHisProProLeuProValLysArgLysCys***GluGluCys 380
Db 1090 GAGACGATGAGGATGACCCCTCCGATCCGTTGATCCGAGATCATCGAGATCATGAGAGAATGC 1149
Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1150 GAGGTCAACGGGTACACGATTCGAATAGCCAGAGATCATGATCAACGCTGTGCTCCAT 1209
Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1210 GTTAGGAATCCTCTCTACTGGGAAACCCGAGACCTTTGGCCCGAAGGTTT----- 1263
Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
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Db 1264 -----GACCAGTCTCAGAGGATTTTCATGGAAACGATTTTCGAGTTTCATC 1308
Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1309 CCATTTGGAGCTGGAAGAAGATCTGCCCCGTTTGAATTTCCGGTTTGGCAATGTTGAG 1368
Qy 461 ThrLeuLeuAlaSerLeuileGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
Db 1369 GTCCATTGGCACAGCTTCTTACCACTTCGACTGGAAGTTGGCGGAAGGAATGAACCT 1428
Qy 478 GlnGlyGlnileLeuLysGly***AspAlaLysValSerMetGluGluAtgAlaGlyLeu 497
Db 1429 -----TCCGATATGACATGTCTGAGGCGAAGGCTT 1461
Qy 498 ThrValProArgAlaHisSerLeuValCysValPro 509
Db 1462 ACCGGAATAAGAAGAACATCTTCTACTGTTCCC 1497

RESULT 15
US-09-292-768-3
; Sequence 3, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: waur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Mentha piperita
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(1518)
; US-09-292-768-3

Alignment Scores:
Pred. No.: 6,69e-75 Length: 1665
Score: 616.50 Matches: 145
Percent Similarity: 47.76% Conservative: 90
Best Local Similarity: 29.47% Mismatches: 206
Query Match: 25.81% Indels: 51
DB: 3 Gaps: 11

US-09-857-581B-66 (1-521) x US-09-292-768-3 (1-1665)
Qy 35 ProProSerPro***ProArgLeuProPheileGlyHis***HisLeuLeuLysAspLys 54
Db 124 CTTCCGGGCGCG--CCGAAGCTGCGCTGATCGGACCTCCACCTCTTATGGGGAAG 180
Qy 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db 181 CTGCGCAGCAGCAGCGTGGCCAGGTGGCGAAGCAGTACGCGCCAGTGGCGCACGTCGAG 240
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuGln 94
Db 241 CTGCGCAGGTGTCTCCGTCTGCTCTCCGCGAGGCCAGGAGGCGCATGAAG 300
Qy 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 301 CTGCTGGAC---CCGGCTCGCGGACCGGTTTCGAGAGCATCGGAGCAGAGATCATGTGG 357
Qy 115 TyrAsp-----ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
Db 358 TACGACAAACGACGACATCATCTTTCAGCCCTTACAGCGTGCACATCGCGCCAGATCGGAAG 417
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Qy 134 LeuileMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 418 ATCTGCTCTCCGAGCTCTCAGCGCCGCAACCTCCGCTCTTCGGCTTCATCAGGCAG 477
Qy 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 478 GACGAGGTGTCCTCCCTCCGACCTCCGCTCTCCGCGCGCGGGGAGGCCGTG 537
Qy 174 Asp***ThrGluGluLeuLeuLysTyr***AsnSerThr***SerMetMet***LeuGly 193
Db 538 GACCTCAGGAGCGGATAGGACGCTGACGTGCTCCATCATCTGCAGCGCGGCTTCGGG 597
Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle*** 209
Db 598 AGCTGTATCAGGAGACGACGAGGAGCTGTGTGAGTGTGTGAAGACGCCCTCAGCATGGCG 657
Qy 210 GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
Db 658 TCGGGTTCGAGCTCGCGGACATGTTCCTCCCTCCCAAGCTCCTCACTTGCTGCTGG 717
Qy 225 -----LysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPheAsp 241
Db 718 AACAGAGCAAGCTGTGGAGGATGCGCGCGGCTCGACGCCATCTCTGAGGCCATC--- 774
Qy 242 ProValValGluArgValIleLysLysArgArg***IleValArgArg***AsnGly 261
Db 775 ---GTGAGGAGCACAAGCTCAGAAG----- 798
Qy 262 Glu*****GluGlyGlu***SerGlyVal---LeuAspThrLeuLeuGluPheAla 280
Db 799 -----ACGCGGAGTTTGGCGGAGGACATATTGACGTACTCTTAGGATCCAG 849
Qy 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
Db 850 AAGGATAGCCAGATCAAGTCCCATCCACCAACGCCATCAAAAGCCTTCATCTTCGAC 909
Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
Db 910 ACGTCTCAGCGGGACCGAGACATCATCAACCAACCCCTGTGGGTGATGGCGGAGCTG 969
Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
Db 970 ATGAGGAATCCAGAGGTGATGGCGAAGCGCAGCGAGGTGAGAGCGCGCTGAAGGGG 1029
Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1030 AAGACGAGCTGGGACGTGGACGACGTGACGAGCTTAAGTACATGAATCGTGTGAAG 1089
Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
Db 1090 GAGACGATGAGGATGACCCCTCCGATCCGTTGATCCCGAGATCATCGAGAGAAGATGC 1149
Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1150 GAGGTCAACGGGTACAGATTCCGATAAGCCAGAAATCATGATCAACGTGTGTCATG 1209
Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1210 GTAGGAATCCTCTCTACTCGGAAAAACCCGAGACCTTTTGGCCCGAAAGGTTT----- 1263
Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db 1264 -----GACCAGTCTCGAGGATTTTCATGGAAACGATTTTCGAGTTCATC 1308
Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1309 CCATTTGGAGCTGGAAGAATCTGCCCGGTTTGAATTCGGGTGGCAATGTTGAG 1368
Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
Db 1369 GTCCCATTTGCAACAGCTTCTTACCCTTCGACTGGAAGTTGGCGGAAGGAATGAACCCCT 1428
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Qy 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeu 497
Db 1429 -----TCCGATATGGACATGTCTGAGGCGAAGGCCTT 1461
Qy 498 ThrValProArgAlaHisSerLeuValCysValPro 509
Db 1462 ACCGGAATAAGAAAGAACATCTTCTACTCGTTCCC 1497
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Search completed: April 29, 2005, 19:13:30
Job time : 305 secs